

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 10:58:36 ; Search time 2197 Seconds
(without alignments)
9864.141 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgcc.....atcaggaaagtggaatcgaaa 500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
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38: em_sv:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	500	100.0	500	6	AX431553	AX431553 Sequence
C 2	490.4	98.1	309400	6	AX127153	AX127153 Sequence
C 3	490.4	98.1	325851	1	AP005283	AP005283 Coryneb
C 4	264	52.8	1776	6	AX123295	AX123295 Sequence
C 5	264	52.8	1776	6	BD165412	BD165412 Novel pol
6	112	22.0	1084	6	AX763278	AX763278 Sequence
7	100	20.0	1065	6	AX065003	AX065003 Sequence
C 8	61.2	12.2	302070	1	AP005223	AP005223 Coryneb
C 9	40.8	8.2	170712	9	AC091879	AC091879 Homo sapi
C 10	40.8	8.2	198687	9	AC093298	AC093298 Homo sapi
C 11	40.2	8.0	147820	9	AC092837	AC092837 Homo sapi
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C 18	38	7.6	79080	2	AC112392_4	Continuation (5 of
C 19	38	7.6	312135	2	AC123341	AC123341 Rattus no
C 20	38	7.6	344264	2	AC098257	AC098257 Rattus no
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C 34	36.4	7.3	2000	6	AX832458	AX832458 Sequence
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C 36	36.4	7.3	5618	8	YSCVPS15	M59835 S.cerevisia
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C 42	36.2	7.2	123236	9	AL590673	AL590673 Human DNA
C 43	36.2	7.2	145746	5	AL953858	AL953858 Zebrafish
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C 45	36.2	7.2	230977	2	AC137883	AC137883 Mus muscu

ALIGNMENTS

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AX431553
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AX431553
Sequence 7 from Patent WO0240679.
AX431553
AX431553.1 GI:21656357
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
Craffon, C.M. and Rayapati, P.J.
Nucleotide sequences for transcriptional regulation in
Corynebacterium glutamicum

AX431553
Sequence 7 from Patent WO0240679.
AX431553
AX431553.1 GI:21656357
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
Craffon, C.M. and Rayapati, P.J.
Nucleotide sequences for transcriptional regulation in
Corynebacterium glutamicum

JOURNAL Patent: WO 0240679-A 7 23-MAY-2002;
CRAFTON COREY M (US); RAYAPATI P JOHN (US)
FEATURES Location/Qualifiers
source 1..500
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Db 481 ATCAGGAAGTGGATCGAAA 500

RESULT 2

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LOCUS AX127153 Sequence 7069 from Patent EP1108790.
DEFINITION AX127153 AX114121
ACCESSION AX127153.1 GI:14041141
VERSION AX127153.1
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
TITLE Novel polynucleotides
JOURNAL Patent: EP 1108790-A 7069 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
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/note="Seq 1 to long (3,309,400) split in 11, seq 7069

3,000,001 3,309,400 309,400"

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Best Local Similarity 98.8%; Pred. No. 3e-137;
Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 113470 ATCCGGGACAGCTCTGCTGATTTCTGAGCTCTTGTGGGTTGTCCGGTTAGGGAA 113411
Qy 481 ATCAGGAAGTGGATCGAAA 500
Db 113410 ATCAGGAAGTGGATCGAAA 113391

RESULT 3

AP005283/c 325651 bp DNA linear BCT 08-AUG-2002
LOCUS AP005283 Corynebacterium glutamicum ATCC 13032 DNA, complete genome, section 10/10.
DEFINITION AP005283 AP005283.1 GI:21325571
ACCESSION AP005283 BA000036
VERSION AP005283.1
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
AUTHORS Nakagawa, S.
TITLE Complete genomic sequence of Corynebacterium glutamicum ATCC 13032
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 325651)
AUTHORS Nakagawa, S.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hako Kogyo Co.
Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,
Tokyo 194-8533, Japan (E-mail:snakagawa@exanagen.com,
Tel:81-44-829-3031, Fax:81-44-813-1851)
COMMENT This sequence is conducted by collaboration of Kyowa Hako Kogyo
Co. Ltd. And Kitasato University.
LOCATION/Qualifiers
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PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC
G01N33/566,
PC G01N33/569 G01N33/700//C12P21/08, (C12N1/21, C12R1/15),
PC (C12N1/21, C12R1/13), (C12N1/21, C12R1/01), (C12P13/08, C12R1/15),
PC C12N15/00,
PC C12N5/00, C12N15/00
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FH Key Location/Qualifiers
FT source 1..1776
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FEATURES

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Query Match 52.8%; Score 264; DB 6; Length 1776;
Best Local Similarity 98.2%; Pred. No. 8e-69;
Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAAACAGCAGGTTAGCGGCTTAACCCACACACGCTTTCGGCAACAATGACGCGAGAGA 60
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DB 212 GCCCACCACATTCGATTTCCGCTCCGATAAAGCCAGCGCCCATATTTTCAGGAGGATT 153
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DB 152 CGCTCGGTTGGCGACATTCGGATCCCGGAAACAGCTCTGCAATGACCTGCGCGCG 93
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QY 181 AGGGAAGCAGCTGGTGCAGGTTTATGTCGGGTTTAAAGCTTCCAGGCGAGTG 240
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DB 92 AGGGAAGCAGCTGGTGCAGGTTTATGTCGGGTTTAAAGCTTCCAGGCGAGTG 33
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QY 241 AGCAAGACGCTAGTCTGGGAGCGCAACCAT 272
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DB 32 AGCAGACGCTAGTCTGGGAGCGCAACCAT 1
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RESULT 6

AX763278
LOCUS 1084 bp DNA linear PAT 25-JUN-2003
Sequence 95 from Patent WO03040291.
ACCESSION AX763278
VERSION AX763278.1 GI:32257846
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Corynebacteriaceae; Corynebacterium.

REFERENCE

1 Zelder, O., Pompejus, M., Schroeder, H., Kroeger, B., Kloppe, C. and
Haberhauer, G.
Genes encoding for carbon metabolism and energy-producing proteins
Patent: WO 03040291-A 95 15-MAY-2003;
JOURNAL BASF AKTIENGESSELLSCHAFT (DE)
Location/Qualifiers
1..1084
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/mol_type='unassigned DNA'
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101..1057
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FEATURES

CDS

101..1057
/note='unnamed protein product; RXA02694'
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RYMLGELYEAPSSVHAYIIGEHGDTLPVLSSATAGVSLSRMLDKDPELEGRLEKI
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GTPAVNRRGIRRVVELEITDHEMERFKHSANTLREIQKQFF"

ORIGIN

Query Match 22.4%; Score 112; DB 6; Length 1084;
Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 TAATCGGCGCATAAATTAAAGGTGTACAAAGGAATCCGGGCACAAAGCTCTTGCTGATTTTC 448
|||||
DB 1 TAATCGGCGCATAAATTAAAGGTGTACAAAGGAATCCGGGCACAAAGCTCTTGCTGATTTTC 60
|||||

QY 449 TCAGCTGCTTTTGTGGTTCGCGTTAGGAAATCAGGAAGTGGGATCGAAA 500
|||||
DB 61 TGAGCTGCTTTTGTGGTTCGCGTTAGGAAATCAGGAAGTGGGATCGAAA 112
|||||

RESULT 7

AX065003
LOCUS 1065 bp DNA linear PAT 24-JAN-2001
Sequence 129 from Patent WO0100844.
ACCESSION AX065003
VERSION AX065003.1 GI:12542715
KEYWORDS
SOURCE
ORGANISM
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacteriineae; Corynebacteriaceae; Corynebacterium.

REFERENCE

1 Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberhauer, G.
Corynebacterium glutamicum genes encoding proteins involved in
carbon metabolism and energy production
Patent: WO 0100844-A 129 04-JAN-2001;
JOURNAL BASF AKTIENGESSELLSCHAFT (DE)
Location/Qualifiers
1..1065
/organism='Corynebacterium glutamicum'
/mol_type='unassigned DNA'
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101..1045
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GELYEAPSSVHAYIIGEHGDTLPVLSSATAGVSLSRMLDKDPELEGRLEKI
FEDTRDAAYHIIDAKGSTSYGIMGLARITRAILQNDVAVPVSAALLHGEYGEEDIYI
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FEATURES

CDS

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GELYEAPSSVHAYIIGEHGDTLPVLSSATAGVSLSRMLDKDPELEGRLEKI
FEDTRDAAYHIIDAKGSTSYGIMGLARITRAILQNDVAVPVSAALLHGEYGEEDIYI
GTPAVNRRGIRRVVELEITDHEMERFKHSANTLREIQKQFF"

ORIGIN

Query Match 20.0%; Score 100; DB 6; Length 1065;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATAAAGGTGTAAACAAAGGAATCCGGGCACAAAGCTCTTGCTGATTTTCGAGCTGTTTG 60
|||||

QY 461 TGGGTTCGCGTTAGGAAATCAGGAAGTGGGATCGAAA 500
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DB 61 TGGGTTCGCGTTAGGAAATCAGGAAGTGGGATCGAAA 100
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RESULT 8

AP005223/c
LOCUS 302070 bp DNA linear BCT 24-JUL-2003
DEFINITION Corynebacterium efficiens YS-314 DNA, complete genome, section
10/11.

ACCESSION	AP005223	BA000035	
VERSION	AP005223.1	GI:23494433	
KEYWORDS	Corynebacterium efficiens YS-314		
SOURCE	Corynebacterium efficiens YS-314		
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.		
REFERENCE	1. Nishio, Y., Nakamura, Y., Kawarabayashi, Y., Usuda, Y., Kimura, E., Sugimoto, S., Matsui, K., Yamagishi, A., Kikuchi, H., Ikeo, K. and Gotohori, T.		
AUTHORS	Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens		
TITLE	Genome Res. 13 (7), 1572-1579 (2003)		
JOURNAL	22723752		
MEDLINE	12840036		
PUBMED	2 (bases 1 to 302070)		
REFERENCE	Kawarabayashi, Y., Yamazaki, J., Hino, Y., Kikuchi, H. and		
AUTHORS	Director-General of Biotechnology Center.		
TITLE	Submitted (17-MAY-2002) Director-General of Biotechnology Center,		
JOURNAL	National Institute of Technology and Evaluation, Biotechnology		
COMMENT	Center; Nishihara 2-49-10, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:biomnate.go.jp, Tel:81-3-3481-1933, Fax:81-3-3481-8424)		
	Kawarabayashi, Y. is officially affiliated with the National		
	Institute of Advanced Industrial Science and Technology, Tsukuba,		
	Ibaraki, 305-8566 Japan		
	Nakamura, Y., Ikeo, K., Suzuki, M. and Mashima, J. are at the		
	National Institute of Genetics, Mishima, Shizuoka, 411-8540 Japan		
	Icho, T. is at the Japan Biological Information Research Center,		
	Koto-ku, Tokyo, 135-0064 Japan		
	Yamagishi, A. is at Tokyo University of Pharmacy and Life Science,		
	Hachioji, Tokyo, 192-0392 Japan		
	Nishio, Y., Usuda, Y. and Sugimoto, S. are at the Ajinomoto Co.,		
	Inc., Kawasaki, Kanagawa, 210-8681 Japan		
	The other authors are at the National Institute of Technology and		
	Evaluation, Shibuya-ku, Tokyo, 151-0066 Japan.		
FEATURES	Location/Qualifiers		
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	ALTAIVKVAEYIGIRYFGHGHSHYVSSKVDLMDKPAEINITITFHIGNGSMAA		
	VGKGVADVSMGTPLAGLVMTGRTDIDFGVPHLARNAMSIDEDINLNKKSQVK		
	GLSGVDVRELHQMIEDGQDWSAYNIYIHLRRYLGSYVALGRVDCLVFTAGVE		
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	DKLKAVRNHGNLPPVMSAALFENMLKRAKEQAHIVLPEGEDDRILMAAHOLLEKO		
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Best Local Similarity 65.2%; Pred. No. 1.3e-06; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 2 AAACAGCCAGGTAGCGGTGTAACCCACCGGTTTCGGCAACAATGACGCGAGAGAG 61
Db 180389 ACACCGGAGGTGACCGCGGTGACCCACCGCGGGGACGCGAGGTGACAGTG 180330
QY 62 CCCACACATTCGGATTCCGTCGATTAAGCCAGCGCCCATATTTGCGAGGAGATTC 121
Db 180329 CCCACAGGTGGCCATCTCCGACGAGCGCGCGCCCATGCGCGCGGAGATCC 180270
QY 122 GCTCGGTTTGGCGACA 139
Db 180269 GCGCGGAGCGCGGCA 180252
RESULT 9
AC091879
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-3136G21, complete sequence.
AC091879 170712 bp DNA linear PRI 21-FEB-2002

AC091879
AC091879.2 GI:18854959
VERSION
HTG.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 170712)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS
Direct Submission
TITLE
Unpublished
JOURNAL
2 (bases 1 to 170712)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
JOURNAL
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
3 (bases 1 to 170712)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS
Direct Submission
TITLE
Submitted (21-FEB-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL
Drive, Walnut Creek, CA 94598, USA
COMMENT
On Feb 21, 2002 this sequence version replaced gi:14333815.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
Query Match 8.2%; Score 40.8; DB 9; Length 170712;
Best Local Similarity 53.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 280 CATCTGGCAGCAGCATGCAATCTGCGAGGCATAGATTGCTTTCGATTTTACAAAT 339
Db 163012 CTTCCTAGCAAAATCTTACATAAATCAGAGAGATTGTATTCTATCTTCAAG 163071
QY 340 GTGATTTTTCACAAAATAACACTTGTCTGACCAATTTTCGACATATCGGGCAT 399
Db 163072 GTGCTTAAAGGAAAAAAGGACAATCTCAAATTTTGTATTTCGAGATAAGCTTCAT 163131
QY 400 AATTAAAGGTGTAACAAAGGAATCCGGGCACAAAGCTCTTGCTGA 443
Db 163132 AATGAGGAGNAACAAAGTCTTTCCAGACAAACAATGCTGA 163175
RESULT 10
AC093298/c
LOCUS
AC093298 198687 bp DNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-543J14, complete sequence.
AC093298
AC093298.3 GI:22038509
VERSION
HTG.
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 198687)
DOE Joint Genome Institute and Stanford Human Genome Center.
AUTHORS
Direct Submission
TITLE
Unpublished
JOURNAL
2 (bases 1 to 198687)
DOE Joint Genome Institute.
AUTHORS
Direct Submission
TITLE
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
JOURNAL

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 198687)
 DOE Joint Genome Institute.
 Direct Submission

Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 198687)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Aug 1, 2002 this sequence version replaced gi:19224834.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sngc.stanford.edu

Quality: Phrap Quality >=40.99.7% of Sequence;

Estimated Total Number of Errors is 0.4.

Location/Qualifiers

1. 198687

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-543L14"

TITLE
 JOURNAL

COMMENT

Direct Submission
 Submitted (09-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jan 9, 2002 this sequence version replaced gi:15341615.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

Center project name: H_NH0137J09

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
 McPherson, Department of Genetics, Washington University, St. Louis
 MO. For additional information about the map position of this
 sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tareno, M., Catanesi, J.J. and de Jong, P.J. (1998). An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
 and coworkers at the Roswell Park Cancer Institute
 (http://bacpac.med.buffalo.edu)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-432012, 2000 bp overlap.
 Actual start of this clone is at base position 1 of RP11-137J9.

Polymorphisms have been identified between AC092837 and AC023468.

There is a transposon in the vector sequence.

FEATURES
 source

1. 147820

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/mol_type="genomic DNA"

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/map="2"

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257. 651

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868. 996

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1308. 1608

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3976. 3998

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3990. 4040

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4041. 4626

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4627. 5225

/rpt_family="L1"

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 198687)
 DOE Joint Genome Institute.
 Direct Submission

Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 198687)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (01-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Aug 1, 2002 this sequence version replaced gi:19224834.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sngc.stanford.edu

Quality: Phrap Quality >=40.99.7% of Sequence;

Estimated Total Number of Errors is 0.4.

Location/Qualifiers

1. 198687

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="RP11-543L14"

REFERENCE
 AUTHORS

TITLE

JOURNAL

REFERENCE
 AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
 source

ORIGIN

Query Match 8.2%; Score 40.8; DB 9; Length 198687;

Best Local Similarity 53.0%; Pred. No. 2;

Matches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 280 CATCTGGCAGCAGCATGCACAATTCGTCAGGCGCATAGATTGGTTTTCGTCGATTACAAT 339

Db 196988 CTTCCTAGCAGAAATCTTACAAATAATCAGAAGAGATTGTATCTTCTTCTCAAG 196929

Qy 340 GTGATTTTTCACAAAATAAATCACTTGGTCTGCACCAATTTTCGGACATATCGGCAT 399

Db 196928 GTGCTTAAAGGAAAAAAGACAAATCTCAATTTTGTATTTTTCGCAATAAGCTTCAT 196869

Qy 400 AATTAAAGTGTACAAAGGAATCCGGCACAAGCTCTTGTCTGA 443

Db 196868 AATGAAGGAGAAACAAAGTCTTCCGACACAAACAAATGCTGA 196825

RESULT 11
 AC092837/c 147820 bp DNA linear PRI 09-JAN-2002

LOCUS AC092837 Homo sapiens BAC clone RP11-137J9 from 2, complete sequence.

DEFINITION AC092837

AC092837.5 GI:18098562

VERSION HTG.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 147820)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence

Genome Res. 8 (11), 1037-1108 (1998)

99063792

PUBMED 9847074

2 (bases 1 to 147820)

Holmes, A., Boyer, E. and Meyer, R.

The sequence of Homo sapiens BAC clone RP11-137J9

Unpublished (2001)

3 (bases 1 to 147820)

Waterston, R.H.

Direct Submission

Submitted (30-JUL-2001) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

4 (bases 1 to 147820)

Waterston, R.

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repeat_region 8628..8664
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repeat_region 9004..9049
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repeat_region 28935..29001
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repeat_region 29018..29235
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Best Local Similarity 56.4%; Pred. No. 2.8;
Matches 75; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 323 TTTGCTCGATTACAAATGATTTTCAACAAATAACACTTGTGCTGACCACTTTT 382
Db 142890 TATTTAGATPAATAATACATTTATAAAATATATACACTTGTTCARATATCTT 142831

QY 383 CGACATATCGGGCATATTAAGGTGPAACAAAGGAATCCGGGCACAAAGCTTTGCTG 442
Db 142830 GGGAAAGGAATGGGCATTGCTATATATGAACAAATCAGCTGAGTTAGTAATTGTTG 142771

QY 443 ATTTTCTGAGCTG 455
Db 142770 ATGCTGAGCGATG 142758

RESULT 12
AC004193
LOCUS Homo sapiens clone UMG:Y23c142 from 6p21, complete sequence.
DEFINITION AC004193
ACCESSION AC004193
VERSION AC004193.1 GI:3980471
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 38194)
AUTHORS Janer, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and
Geraghty, D.E.
TITLE Large scale sequence analysis of the human MHC class I region
JOURNAL Unpublished (1998)
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 38194)
AUTHORS Geraghty, D.E. and Olson, M.V.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Human Genome Center, University of
Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 38194)
AUTHORS Geraghty, D.E. and Olson, M.V.
TITLE Direct Submission
```


Fri Aug 6 10:32:28 2004

Db 25685 CAAGGTAGAGGGCGAGGACAGGAGGTGCGCGGATTCGGACCCCTCCCAACCACC 25626
 Qy 227 CCAGGCGAGTGGTGAAGCAAGCGCTAGTCTGGGGAGCGAACCACATATTGAG 278
 Db 25625 GCCCATGGCGGGGAGGAGACTACCGACCGAAGCGGACCGAGAACGAG 25574

RESULT 15

AB023057 81561 bp DNA linear PRI 20-NOV-1999
 LOCUS Homo sapiens genomic DNA, chromosome 6p21.3, HLA class I region,
 clone:779F20, complete sequence.

ACCESSION AB023057

VERSION AB023057.1 GI:5672626

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Shiina,T., Tamiya,G., Oka,A., Takishima,N., Yamagata,T.,
 Kikawa,E., Iwata,K., Tomizawa,M., Okuaki,N., Kuwano,Y.,
 Watanabe,K., Fukuzumi,Y., Itakura,S., Sugawara,C., Ono,A.,
 Yamazaki,M., Tashiro,H., Ando,A., Ikemura,T., Soeda,E., Kimura,M.,
 Bahram,S. and Inoko,H.
 Molecular dynamics of MHC genesis unraveled by sequence analysis of
 the 1.796.938-bp HLA class I region

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13282-13287 (1999)

MEDLINE 20027539

PUBMED 10557312

REFERENCE

2 (bases 1 to 81561)

Shiina,T. and Takishima,N.

Direct Submission

Submitted (29-JAN-1999) Takashi Shiina, Tokai University School of

Medicine, Department of Molecular Life Science 2; Bohseidai,

Isehara, Kanagawa 259-1193, Japan

(E-mail:tshiina@is.icc.u-tokai.ac.jp, Tel:81-463-93-1121,

Fax:81-463-94-8884)

Location/Qualifiers

1..81561

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/clone="779F20"

FEATURES

ORIGIN

Query Match 7.7%; Score 38.4; DB 9; Length 81561;
 Best Local Similarity 47.8%; Pred. NO. 8.8;
 Matches 111; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 47 ATGACGGCGAGAGACCCACCATTCGCTCGGATTCGCTCGGATTAAGCGCGCCCATAT 106
 Db 52642 AGGCCGCGGGACAGCCCCACCGCGGAGAGGGGCTGCCAAAAGGCAACAGCCATAG 52701

Qy 107 TTGCAGGAGGATTTCGCTCGGTTTGGCGACATTCGGATCCCGGAAACAGCTCTGCAA 166
 Db 52702 GAGATGAGCAGGGGTGCTGCTCGCTCGGAGACTCATCTCCCAACCCACCGACGCCA 52761

Qy 167 TGACCTGCGCGCGAGGAG 226
 Db 52762 CAAGGTAGAGGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 52821

Qy 227 CCAGGCGAGTGGTGAAGCAAGCGCTAGTCTGGGGAGCGAAACCATATTGAG 278
 Db 52822 GCCCATGGCGGGGAGGAGACTACCGACCGAAGCGGACCGAGAACGAG 52873

Search completed: August 4, 2004, 12:43:55
 Job time : 2202 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 10:57:06 ; Search time 303 Seconds
(without alignments)
7010.228 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
Sequence: 1 aaacagccaggttagcgccg.....atcaggagtggtggtcgaa 500

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	500	100.0	500	6	ABQ73179	Abq73179 C. glutam
2	490.4	98.1	309400	5	AAH68534	Aah68534 C. glutam
3	264	52.8	1776	5	AAH68176	Aah68176 C. glutam
4	264	52.8	1776	7	ACA01190	Acad01190 C. glutam
5	112	22.4	1084	9	ADD13410	Add13410 C. glutam
6	100	20.0	1065	4	AAF71424	Aaf71424 Coryneb
7	36.4	7.3	1263	9	ADC90725	Adc90725 B. faeciu
8	36.4	7.3	2000	7	ACC61930	Acc61930 Gene sequ
9	36.2	7.2	1053	7	ACA42017	Aca42017 Prokaryot
10	34.8	7.0	6210	2	AXX02986	Aax02986 Human li-
11	33.2	6.6	4613	4	ABU11796	Abu11796 Drosophil
12	32.8	6.6	32191	4	AAS30497	Aas30497 DNA encod
13	32.8	6.6	32191	4	AAL06277	Aal06277 Human rep
14	32.8	6.6	46107	4	AAK71730	Aak71730 Human imm
15	32.6	6.5	257	6	ABN16341	Abn16341 Human ORF
16	32.4	6.5	579	6	ABN62193	Abn62193 Human can
17	32.4	6.5	1666	6	ABQ34526	Abq34526 Oligonuc
18	32.4	6.5	1666	6	ABQ34527	Abq34527 Oligonuc
19	32.2	6.4	3108	6	ABN59617	Abn59617 Novel hum
20	32.2	6.4	3690	9	ADC37644	Adc37644 Human nuc
21	32	6.4	577	4	AAI42479	Aai42479 Probe #11
22	32	6.4	577	4	ABS36372	Abs36372 Human liv
23	32	6.4	577	6	ABS10712	Abs10712 Human gen

C	24	32	6.4	2000	7	ADA71938	Ada71938 Rice gene
C	25	31.8	6.4	1295	7	ACD93559	Acad93559 Human col
C	26	31.8	6.4	1308	7	ACA43692	Aca43692 Prokaryot
C	27	31.6	6.3	666	8	ADB07101	Adb07101 Allostoc
C	28	31.6	6.3	2625	3	AAE60048	Aae60048 Human sec
C	29	31.6	6.3	2625	7	ADA97959	Ada97959 Human sec
C	30	31.6	6.3	2625	7	ADA43865	Ada43865 Human sec
C	31	31.6	6.3	2625	9	ADC20114	Adc20114 Human sec
C	32	31.6	6.3	19403	4	ABU11856	Abu11856 Drosophil
C	33	31.6	6.3	57130	7	ABQ77243	Abq77243 Human MAR
C	34	31.6	6.3	110000	8	ADB12064	Adb12064 (3 of
C	35	31.4	6.3	636	7	ACF68771	Acf68771 Phototrab
C	36	31.4	6.3	848	2	AAZ17390	Aaz17390 Human gen
C	37	31.4	6.3	2512	7	ABZ35845	Abz35845 Human sec
C	38	31.4	6.3	3923	7	ABX08775	Abx08775 Angiogene
C	39	31.4	6.3	24526	6	ADA43979	Ada43979 Human tra
C	40	31.4	6.3	26565	6	ABS78924	Abs78924 E. coli C
C	41	31.4	6.3	110000	7	ACF67367	Acf67367 (16 o
C	42	31.4	6.3	249878	7	ACF65381	Acf65381 Phototrab
C	43	31.2	6.2	536	9	ADB68842	Adb68842 Minority
C	44	31.2	6.2	629	6	ABQ53668	Abq53668 Oligonuc
C	45	31.2	6.2	629	6	ABQ53669	Abq53669 Oligonuc

ALIGNMENTS

RESULT 1
ABQ73179
ID ABQ73179 standard; DNA; 500 BP.
XX
AC ABQ73179;
DT
DT 27-SEP-2002 (first entry)
XX
DE C. glutamicum transcriptional regulatory region ldh DNA SEQ ID NO:7.
XX
KW Corynebacterium glutamicum; gene expression;
KW amino acid biosynthesis; gene; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200240679-A2;
XX
PD 23-MAY-2002.
XX
PF 15-NOV-2001; 2001WO-US043096.
XX
PR 15-NOV-2000; 2000US-0248219P.
XX
PA (RAYA/) RAYAPATI P J.
PA (CRAP/) CRAFTON C M.
PI Rayapati PJ, Crafton CM;
XX
XX WPI; 2002-575217/61.
XX
PT Novel polynucleotides from Corynebacterium glutamicum useful for inducing
PT and regulating expression of genes, including those that are involved in
PT amino acid biosynthesis, in bacterial cells.
XX
XX Claim 20; Page 25; 112pp; English.

The present invention describes Corynebacterium glutamicum transcriptional regulatory region polynucleotide sequences (I). ABQ73173 to ABQ73194 represent the C. glutamicum transcriptional regulatory regions pta, aceA, aceB, adh, aldB, poxB, ldh, amyE, malZ, bglX, gam, glxK, hisD, pyrR, purD, hrcA, htpX, dnaK, etc, grpE, and narX, respectively. (I) can be used for producing a vector. (I) can also be used for producing a transformed Corynebacterium sp. host cell, which is useful for producing a biosynthetic product. (I) is useful for producing a Corynebacterium sp. host cell, which is useful for producing an amino acid. (I) is useful for regulating and enhancing the production of a

CC variety of products in host cells, including amino acids such as lysine,
 CC purine nucleotides such as inosinic acid, and heterologous polypeptides
 XX
 SQ Sequence 500 BP; 127 A; 110 C; 145 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 3.9e-155;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAACAGCCAGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGCGAGAGA 60
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 Qy 61 GCCCACCACATTCGATTTCGGTCCGATAAAGCCAGCGCCATATTTGACGGAGGATT 120
 Db 61 GCCCACCACATTCGATTTCGGTCCGATAAAGCCAGCGCCATATTTGACGGAGGATT 120
 Qy 121 CGCTCGGTTTGGCGACATTCGGATCCCGGAACCGACTCTGCAATGACCTGCGCGCG 180
 Db 121 CGCTCGGTTTGGCGACATTCGGATCCCGGAACCGACTCTGCAATGACCTGCGCGCG 180
 Qy 181 AGGGAAGCGAGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Db 181 AGGGAAGCGAGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Qy 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTGAGTCATCTTGGCAGAGCATGCACA 300
 Db 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTGAGTCATCTTGGCAGAGCATGCACA 300
 Qy 301 ATCTCGAGGCGATAGATTGGTTTGTGTCGATTTACAAATGATTTTTCACAAAATA 360
 Db 301 ATCTCGAGGCGATAGATTGGTTTGTGTCGATTTACAAATGATTTTTCACAAAATA 360
 Qy 361 ACATTTGTCGACACATTTTCGGACATATTCGGGACATAATCGGGCATATTAAGGTGTAACAAAGGA 420
 Db 361 ACATTTGTCGACACATTTTCGGACATATTCGGGACATAATCGGGCATATTAAGGTGTAACAAAGGA 420
 Qy 421 ATCCGGGACAAAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Db 421 ATCCGGGACAAAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Qy 481 ATCAGGAAGTGGGATCGAAA 500
 Db 481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2
 AAH68534/c
 ID AAH68534 standard; DNA; 309400 BP.

XX AC AAH68534;

XX DT 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 7069.

XX DE Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
 XX KW organic acid synthesis; ds.
 XX KW Corynebacterium glutamicum.

XX OS EP1108790-A2.
 XX PN 20-JUN-2001.

XX PF 18-DEC-2000; 2000EP-00127688.
 XX PR 16-DEC-1999; 99JP-00377484.
 XX PR 07-APR-2000; 2000JP-00159162.
 XX PR 03-AUG-2000; 2000JP-00280988.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX WPI; 2001-376931/40.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 XX Disclosure; SEQ ID NO 7069; 246pp + Sequence Listing; English.

PS The present invention provides a number of nucleotide and protein
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Coryneform bacterium, and identifying a homologue of a gene derived from
 CC Coryneform bacterium. Coryneform bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a nucleic acid described
 CC in the exemplification of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the European Patent Office

XX SQ Sequence 309400 BP; 70133 A; 86477 C; 83115 G; 69675 T; 0 U; 0 Other;

Query Match 98.1%; Score 490.4; DB 5; Length 309400;
 Best Local Similarity 98.8%; Pred. No. 1.6e-150;
 Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AAAACAGCCAGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGCGAGAGA 60
 Db 113890 AAAACAGCCAGTTAGCGGTGTAACCCACACCGTTTCGGCAACATGACGGCGAGAGA 113831
 Qy 61 GCCCACCACATTTGGGATTTCCGCTCCGATAAAGCCAGCGCCATATTTGACGGAGGATT 120
 Db 113830 GCCCACCACATTTGGGATTTCCGCTCCGATAAAGCCAGCGCCATATTTGACGGAGGATT 113771
 Qy 121 CGCTCGGTTTGGCGACATTCGGATCCCGGAACCGACTCTGCAATGACCTGCGCGCG 180
 Db 113770 CGCTCGGTTTGGCGACATTCGGATCCCGGAACCGACTCTGCAATGACCTGCGCGCG 113711
 Qy 181 AGGGAAGCGAGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGTTCGAGCGAGTGGTG 240
 Db 113710 AGGGAAGCGAGTGGTGGCAGGTTTGTAGTGGGGTTTAAAGTTCGAGCGAGTGGTG 113651
 Qy 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTGAGTCATCTTGGCAGAGCATGCACA 300
 Db 113650 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTGAGTCATCTTGGCAGAGCATGCACA 113591
 Qy 301 ATCTCGAGGCGATAGATTGGTTTGTGTCGATTTACAAATGATTTTTCACAAAATA 360
 Db 113590 ATCTCGAGGCGATAGATTGGTTTGTGTCGATTTACAAATGATTTTTCACAAAATA 113531
 Qy 361 ACATTTGTCGACACATTTTCGGACATATTCGGGACATAATCGGGCATATTAAGGTGTAACAAAGGA 420
 Db 113530 ACATTTGTCGACACATTTTCGGACATATTCGGGACATAATTAAGGTGTAACAAAGGA 113471
 Qy 421 ATCCGGGACAAAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 480
 Db 113470 ATCCGGGACAAAGCTCTTGCTGATTTCTGAGCTGCTTTGTGGGTTTTCGGGTTAGGGAA 113411
 Qy 481 ATCAGGAAGTGGGATCGAAA 500
 Db 113410 ATCAGGAAGTGGGATCGAAA 113391

RESULT 3
 AAH68176/c
 ID AAH68176 standard; DNA; 1776 BP.
 XX AC AAH68176;
 XX

DT 26-SEP-2001 (first entry)

XX C glutamicum coding sequence fragment SEQ ID NO: 3211.

XX Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.

XX Corynebacterium glutamicum.

XX EF1108790-A2.

XX 20-JUN-2001.

XX 18-DEC-2000; 2000EP-00127689.

XX 16-DEC-1999; 99JP-00377484.

XX 07-APR-2000; 2000JP-00159162.

XX 03-AUG-2000; 2000JP-00280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Nakagawa S, Mizoguchi H, Ando S, Hayaashi M, Ochiai K, Yokoi H;

XX Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI: 2001-376931/40.

XX P-PSDB; AAG92957.

XX Novel polynucleotides derived from Coryneform bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analyzing
XX expression profile or pattern of a gene and identifying homologous gene.

XX Claim 8; SEQ ID NO 3211; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and analysing
XX the expression profile or expression pattern of a gene derived from
XX Coryneform bacterium, and identifying a homologue of a gene derived from
XX coryneform bacterium. Coryneform bacteria are useful for producing amino
XX acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a nucleic acid, described
XX in the exemplification of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from the European Patent Office

XX Sequence 1776 BP; 365 A; 505 C; 511 G; 395 T; 0 U; 0 Other;

Query Match 52.8%; Score 264; DB 5; Length 1776;
Best Local Similarity 98.2%; Pred. No. 1.5e-76;
Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAAACAGCCAGGTTAGCGGCTGTACCCACACGCTTTCGGCAACAATGACGGCGAGAGA 60

Db 272 AAAACAGCCAGGTTAGCGGCTGTACCCACACGCTTTCGGCAACAATGACGGCGAGAGA 213

QY 61 GCCCACCACATTTGGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTGCAGGGAGGATT 120

Db 212 GCCCACCACATTTGGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTGCAGGGAGGATT 153

QY 121 CGCTCGCGGTTTGGCGACATTCGGATCCCGGAACCACTCTGCAATGACCTGCGCGCG 180

Db 152 CGCTCGCGGTTTGGCGACATTCGGATCCCGGAACCACTCTGCAATGACCTGCGCGCG 93

QY 181 AGGGAAGCGAGTGGTGGCGAGTTTATGTCGGGTTTAAAGCTTGCAGGCGAGTGGTG 240

Db 92 AGGGAAGCGAGTGGTGGCGAGTTTATGTCGGGTTTAAAGCTTGCAGGCGAGTGGTG 33

QY 241 AGCAAGACGCTAGTCTCTGGGAGCGAAACCAT 272

Db 32 AGCAGAGACGCTAGTCTCTGGGAGCGAAACCAT 1

RESULT 5
ADD13410

RESULT 4

ACA01190/c

XX ID ACA01190 standard; DNA; 1776 BP.

XX ACA01190;

XX 03-JUN-2003 (first entry)

XX C. glutamicum derived ORF SEQ ID 1181.

XX Coryneform; nucleic acid array; fermentation; culture; ds.

XX Corynebacterium glutamicum.

XX DE10128510-A1.

XX 19-DEC-2002.

XX 13-JUN-2001; 2001DE-01028510.

XX 13-JUN-2001; 2001DE-01028510.

XX (DEGS) DEGUSSA AG.

XX Farwick M, Moeckel B, Pfefferle W, Bathe B, Huthmacher K;

XX WPI: 2003-279970/28.

XX New nucleic acid array useful for monitoring mRNA expression of
XX Corynebacterium glutamicum during fermentation, comprising nucleic acid
XX from Corynebacterium glutamicum.

XX Claim 1; Page 426-427; 709pp; German.

XX This invention describes a novel nucleic acid array involving
XX Corynebacterium glutamicum polynucleotides. The arrays are used to
XX analyse C. glutamicum, particularly for monitoring a fermentation process
XX to determine expression levels of C. glutamicum cellular mRNA. Such
XX monitoring particularly differentiates between expression levels of
XX different strains of C. glutamicum and allows the adjustment of different
XX culture and fermentation conditions. ACA0010-ACA02188 represent C.
XX glutamicum derived polynucleotides described in the disclosure of the
XX invention

XX Sequence 1776 BP; 365 A; 505 C; 511 G; 395 T; 0 U; 0 Other;

Query Match 52.8%; Score 264; DB 7; Length 1776;
Best Local Similarity 98.2%; Pred. No. 1.5e-76;
Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAAACAGCCAGGTTAGCGGCTGTACCCACACGCTTTCGGCAACAATGACGGCGAGAGA 60

Db 272 AAAACAGCCAGGTTAGCGGCTGTACCCACACGCTTTCGGCAACAATGACGGCGAGAGA 213

QY 61 GCCCACCACATTTGGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTGCAGGGAGGATT 120

Db 212 GCCCACCACATTTGGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTGCAGGGAGGATT 153

QY 121 CGCTCGCGGTTTGGCGACATTCGGATCCCGGAACCACTCTGCAATGACCTGCGCGCG 180

Db 152 CGCTCGCGGTTTGGCGACATTCGGATCCCGGAACCACTCTGCAATGACCTGCGCGCG 93

QY 181 AGGGAAGCGAGTGGTGGCGAGTTTATGTCGGGTTTAAAGCTTGCAGGCGAGTGGTG 240

Db 92 AGGGAAGCGAGTGGTGGCGAGTTTATGTCGGGTTTAAAGCTTGCAGGCGAGTGGTG 33

QY 241 AGCAAGACGCTAGTCTCTGGGAGCGAAACCAT 272

Db 32 AGCAGAGACGCTAGTCTCTGGGAGCGAAACCAT 1

ID ADD13410 standard; DNA; 1084 BP.
 XX ADD13410;
 AC
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE C. glutamicum carbon metabolism associated DNA RXA02694.
 XX
 DE ds; gene; carbon metabolism; energy-rich molecule;
 XX oxidative phosphorylation; fine chemical; amino acid production;
 KW lysine production; nucleotide production; nucleoside production;
 KW lipid production; fatty acid production; diol production;
 KW carbohydrate production; aromatic compound production;
 KW vitamin production; co-factor production; enzyme production; food;
 KW animal feed; cosmetic; pharmaceutical.
 XX
 OS Corynebacterium glutamicum.
 XX
 XX Key Location/Qualifiers
 FT CDS 101..1057
 FT /*tag= a
 XX
 XX WO2003040291-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 31-OCT-2002; 2002WO-EP012135.
 XX
 XX 05-NOV-2001; 2001DE-01054270.
 XX
 XX (BADI) BASF AG.
 XX
 XX Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;
 PI Haberhauer G;
 XX
 XX WPI; 2003-505068/47.
 DR P-PSDB; ADD13411.
 XX
 XX New nucleic acid encoding variant forms of proteins involved in carbon
 PT compound metabolism, useful for production of fine chemicals,
 PT specifically lysine, in microorganisms.
 XX
 XX Claim 1; SEQ ID NO 95; 259pp; German.
 XX
 CC This invention describes novel polynucleotides and polypeptides
 CC associated with the metabolism of carbon compounds and generation of
 CC energy-rich molecules by oxidative phosphorylation in Corynebacterium
 CC glutamicum. The polynucleotides of the invention are isolated from a
 CC nucleic acid library of C. glutamicum then mutated at the specified
 CC positions, cloned and expressed by standard methods. Cells, especially
 CC Corynebacterium glutamicum, containing vectors that express the
 CC polynucleotides are used for production of fine chemicals, preferably
 CC amino acids and specifically lysine, but more generally nucleotides,
 CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, co-factors and enzymes. These are useful in the
 CC food, animal feed, cosmetics and pharmaceutical industries.
 CC polynucleotides, optionally as primers and probes, can also be used for
 CC identification and classification of C. glutamicum and related species,
 CC e.g. for diagnosis; for genomic mapping; functional or evolutionary
 CC studies gene manipulation, and modulation of metabolic activity. Cells
 CC that contain the products of the invention may produce fine chemicals in
 CC better yields, with higher productivity and/or more efficiently.
 XX
 XX Sequence 1084 BP; 270 A; 308 C; 285 G; 221 T; 0 U; 0 Other;
 SQ
 Query Match 22.4%; Score 112; DB 9; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 3.3e-26;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 389 TAATCGGCATAATTAAGGCTGTACAAAGGAATCCGGGCAACGCTTGTGCTGATTTC 448
 DB 1 TAATCGGCATAATTAAGGCTGTACAAAGGAATCCGGGCAACGCTTGTGCTGATTTC 60

QY 449 TGAGCTGCTTTGGGTTGTTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 500
 DB 61 TGAGCTGCTTTGGGTTGTTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 112
 RESULT 6
 AAF71424
 ID AAF71424 standard; DNA; 1065 BP.
 XX
 AC AAF71424;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.
 XX
 XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 XX WO200100844-A2.
 XX
 XX 04-JAN-2001.
 XX
 XX 23-JUN-2000; 2000WO-IB000943.
 XX
 XX 25-JUN-1999; 99US-0141031P.
 XX 08-JUL-1999; 99DE-01031412.
 XX 08-JUL-1999; 99DE-01031413.
 XX 08-JUL-1999; 99DE-01031419.
 XX 08-JUL-1999; 99DE-01031420.
 XX 08-JUL-1999; 99DE-01031424.
 XX 08-JUL-1999; 99DE-01031428.
 XX 08-JUL-1999; 99DE-01031431.
 XX 08-JUL-1999; 99DE-01031433.
 XX 08-JUL-1999; 99DE-01031434.
 XX 08-JUL-1999; 99DE-01031510.
 XX 08-JUL-1999; 99DE-01031562.
 XX 08-JUL-1999; 99DE-01031634.
 XX 09-JUL-1999; 99DE-01032180.
 XX 09-JUL-1999; 99DE-01032227.
 XX 09-JUL-1999; 99DE-01032230.
 XX 09-JUL-1999; 99US-0143208P.
 XX 14-JUL-1999; 99DE-01032324.
 XX 14-JUL-1999; 99DE-01032973.
 XX 14-JUL-1999; 99DE-01033005.
 XX 27-AUG-1999; 99DE-01040765.
 XX 31-AUG-1999; 99US-0151572P.
 XX 03-SEP-1999; 99DE-01042076.
 XX 03-SEP-1999; 99DE-01042086.
 XX 03-SEP-1999; 99DE-01042087.
 XX 03-SEP-1999; 99DE-01042088.
 XX 03-SEP-1999; 99DE-01042095.
 XX 03-SEP-1999; 99DE-01042123.
 XX 03-SEP-1999; 99DE-01042125.
 XX
 XX (BADI) BASF AG.
 XX
 XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
 XX WPI; 2001-061975/07.
 DR P-PSDB; AAB79307.
 XX
 PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 PT metabolism and oxidative phosphorylation protein for production or
 PT modulation of production of fine chemicals e.g. amino acids,
 PT carbohydrates or enzymes.

XX Claim 3; Page 332-333; 1246pp; English.

XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar

CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243

CC to AAB 79633 which are involved in carbon metabolism and energy

CC production. The C. glutamicum SMP gene can be used in vectors (II) for

CC expression in host cells and production or modulation of production of

CC fine chemicals, such as, an organic acid, a proteinogenic or

CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a

CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,

CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a

CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III) of

CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells

CC containing them are used to map genomes of organisms related to C.

CC glutamicum, identify and localise C. glutamicum sequences of interest, in

CC evolutionary studies, in determining SMP protein regions required for

CC function, in modulating SMP protein activity, in modulating the

CC metabolism of sugars, and in modulating high-energy molecule production

CC in a cell (i.e. ATP, NADPH)

XX Sequence 1065 BP; 264 A; 304 C; 279 G; 218 T; 0 U; 0 Other;

XX

Query Match 20.0%; Score 100; DB 4; Length 1065;

Best Local Similarity 100.0%; Pred. No. 3.1e-22;

Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 ATTAAAGGTGTAAACAAAGGAATCCGGCACAGCTCTTCGATTTCTGAGCTGCTTTG 460

DB 1 ATTAAAGGTGTAAACAAAGGAATCCGGCACAGCTCTTCGATTTCTGAGCTGCTTTG 60

QY 461 TGGGTTGTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 500

DB 61 TGGGTTGTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 100

RESULT 7

ADC90725/c

ID ADC90725 standard; DNA; 1263 BP.

XX

AC ADC90725;

XX

AC ADC90725;

XX

DT 01-JAN-2004 (first entry)

XX

DE E. faecium DNA sequence SEQ ID 352.

XX

KW ds; gene; urinary tract infection; bacteraemia; endocarditis; wound;

KW abdominal-pelvic infection.

XX

OS Enterococcus faecium.

XX

PN US6583275-B1.

XX

PN 24-JUN-2003.

XX

PD 30-JUN-1998; 98US-00107532.

XX

PF 02-JUL-1997; 97US-0051571P.

XX

PR 14-MAY-1998; 98US-0085598P.

XX

XX (GENO-) GENOME THERAPEUTICS CORP.

PA Doucette-Stamm LA, Bush D;

XX

PI WPI: 2003-799836/75.

XX

DR P-PSDB; ADC94379.

XX

XX New isolated nucleic acid derived from Enterococcus faecium encoding an

PT Enterococcus faecium polypeptide useful for detection, prevention and

PT treatment of a pathological condition resulting from a bacterial

PT infection.

XX

XX

Example 1; SEQ ID NO 352; 243pp; English.

XX The invention relates to an isolated nucleic acid derived from

CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having

CC one of 10 fully defined sequences given in the (or comprising 40

CC sequential nucleotides chosen from any of the nucleic acids, its

CC complement or sequences hybridising to it). Also included are a

CC recombinant vector comprising the nucleic acid operably linked to

CC transcription regulatory element, a cell comprising the vector and a

CC single-stranded probe comprising the nucleic acid. The nucleic acids are

CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.

CC The nucleic acids is useful for diagnosing pathological conditions

CC resulting from E. faecium bacterial infection (e.g. urinary tract

CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic

CC nucleic acid is useful for recombinant production of Candida albicans -

CC derived peptides or antisense polypeptides. Pharmaceutical compositions

CC and vaccines containing the nucleic acid are useful for preventing or

CC treating Enterococcus faecium infections. The present sequence represents

CC one if the disclosed E. faecium nucleic acids.

XX

Sequence 1263 BP; 338 A; 245 C; 244 G; 436 T; 0 U; 0 Other;

XX

Query Match 7.3%; Score 36.4; DB 9; Length 1263;

Best Local Similarity 53.5%; Pred. No. 0.43;

Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 292 GCATGCACAAATTCGCGAGGCGATAGATTGTTTGTCTCGATTACATGTGATTTTCA 351

DB 293 GCAATCACTAATCCGATGATCAGATTTGTTTGTCTCGATTTCCTAGCAATAAACTA 234

QY 352 ACAAAAATAACACTTGGTCTGACCACATTTTCGGACATAATCGGCATATAAAGGTGT 411

DB 233 CTAATCAAAACAAATAATAGTAGCCATATAAAGAGGAGCGAGCTGTTAATAATTCACAGCA 174

QY 412 AACAAAGGAATCCGGGCAACAG 433

DB 173 GATAAAGAACGGTGGCGATAAG 152

RESULT 8

ACC61930

ID ACC61930 standard; DNA; 2000 BP.

XX

AC ACC61930;

XX

DT 20-JUN-2003 (first entry)

XX

DE Gene sequence #SEQ ID 2642.

XX

KW Multiprotein complex; eukaryote; drug target; diagnosis; gene; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN EP1258494-A1.

XX

PD 20-NOV-2002.

XX

PF 20-DEC-2001; 2001EP-00130253.

XX

PR 15-MAY-2001; 2001EP-00111774.

XX

XX (CELL-) CELLZONE AG.

PA Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;

XX

PI Marzioch M, Schultz JD, Superti-Furga GD;

XX

DR WPI: 2003-250078/25.

XX

DR P-PSDB; ABR53888.

XX

PT New isolated protein complexes useful for diagnosing a disease or

PT disorder, or as a target for an active agent of a pharmaceutical,

PT preferably a drug target in the treatment or prevention of disease or


```

XX 04-AUG-1997; 97US-0054646P.
PR 02-JUL-1998; 98US-0091650P.
XX
PA (MILL-) MILLENNIUM BIOTHEAPEUTICS INC.
XX
XX Pan Y;
XX
DR WPI; 1999-153692/13.
XX
XX New isolated nucleic acid encoding the new human cytokine Tango-77 - used
PT to inhibit inflammation and to screen for specific modulators.
XX
XX Example 5; Fig 3; 226pp; English.
XX
CC AAX02956-X03048 and AAX22301-X22304 are overlapping BAC genomic sequences
CC containing alternatively spliced forms of human IL-1ra. Such fragments
CC are used in the method of the invention which describes the isolation of
CC a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is a
CC member of the cytokine superfamily that is expected to inhibit
CC inflammation by binding to the interleukin-1 receptor (IL-1R). It may
CC also bind to a new receptor so could regulate other cellular processes
CC associated with acute or chronic inflammation, e.g. asthma, chronic
CC myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory
CC bowel disease. It may also induce or suppress interleukins, cytokines and
CC growth factors. Modulators of this protein are used to treat or prevent
CC conditions associated with abnormal levels of inflammation, or activity
CC of IL-1 or its receptor complex
XX
SQ Sequence 6210 BP; 1911 A; 1343 C; 1370 G; 1584 T; 0 U; 2 Other;
Query Match 7.0%; Score 34.8; DB 2; Length 6210;
Best Local Similarity 52.8%; Pred. No. 3.3;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 280 CATCTTGGCAGAGCATGCAAAATTCGACGGGCAATAGATGTTTGTCTCGATTACAAAT 339
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2193 CAGCAGGAAAAAGTATATACATTTTCATAAAGAATAAATACATTCGTCTGAGTTTCTTAC 2252
QY 340 GTGATTTTTCACAAAATACACTTGTCTGACCAATTTTCGGACATAATCGGGCAT 399
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2253 ATATATTTTAAAGTAGTAATACAAATGTTTAGGAACATTTTAAATGCCAACCTC 2312
QY 400 AATTAAAGGTGAACAAAGGAA 421
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2313 ATTAAATATTAGAAGTGAA 2334
RESULT 11
ABLI1796
ID ABLI1796 standard; cDNA; 4613 BP.
XX
AC ABLI1796;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29870.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEXE ) PE CORP NY.
PA
Venter JC, Adams M, Li PWD, Myers EW;
WPI; 2001-656860/75.
P-PSDB; ABB67693.
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions.
Claim 1; SEQ ID NO 29870; 21pp + Sequence Listing; English.
The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
sequences (ABLI01840-ABLI16175) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 4613 BP; 1252 A; 1009 C; 997 G; 1355 T; 0 U; 0 Other;
Query Match 6.6%; Score 33.2; DB 4; Length 4613;
Best Local Similarity 61.6%; Pred. No. 9.6;
Matches 53; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 346 TTTTCAACAAAATAACACTTGGTCTGACCAATTTTCGGACATAATCGGGCATATTA 405
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
461 TTTTCAAGAAATAAACTTTTCTCTCTGTCGACATCAGCGAAAATAATATCGCATTCGGAA 520
QY 406 AGTCTTAACAAAGGAATCGGGCACA 431
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
521 AAGTATAAAATAAAATGAGGACGCA 546
RESULT 12
AAS30497/c
ID AAS30497 standard; DNA; 32191 BP.
XX
AC AAS30497;
XX
DT 21-NOV-2001 (first entry)
XX
DE DNA encoding novel prostate gland antigen, Seq ID No 355.
XX
KW Human; neurotropic; neuroprotective; cytostatic; antiparkinsonian;
KW antianaemic; dermatological; immunosuppressive; antiinflammatory;
KW antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic;
KW osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss;
KW prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy;
KW hyperplasia; carcinoma; prostate neoplastic disorder; skin aging;
KW reproductive system disorder; autoimmune disorder; urinary system;
KW systemic lupus erythematosus; rheumatoid arthritis; cardiovascular;
KW blood-related disorder; hyperproliferative disorder; respiratory;
KW neurological disorder; endocrine disorder; inflammatory disorder;
KW liver disorder; wound healing; food preservative; ds.
XX
OS Homo sapiens.
XX
PN WO200155447-A1.
XX
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001330.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.

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PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209457P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217956P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 08-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233085P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0241826P.
 PR 08-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-476223/51.

XX Novel isolated prostate gland related polypeptide useful for diagnosis
 PT and treatment of disorders of prostate such as prostatodystonia,
 PT prostatitis, prostatitis, benign prostatic hypertrophy and malacoplakia.

XX Claim 1; SEQ ID NO 355; 512pp; English.

XX The invention relates to novel isolated prostate gland related nucleic
 CC acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis,

RESULT 13
AAL06277/c
ID AAL06277 standard; DNA; 32191 BP.
XX
XX AAL06277;
XX AC
XX DT 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 8965.
XX DE
XX Human; reproductive system related antigen; reproductive system disorder;
XX KW cancer; gene therapy; ds.
XX KW
XX
XX Homo sapiens.
XX OS
XX WO200155320-A2.
XX PN
XX PD
XX PF 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001339.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.

RESULT 15

ABN16341
ID ABN16341 standard; cDNA; 257 BP.

XX
XX
AC
ABN16341;

XX
XX
AC
24-JUN-2002 (first entry)

XX
XX
DE
Human ORFX polynucleotide sequence SEQ ID NO:1159.

XX
XX
KW
Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW
hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW
degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW
cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW
hypertension; hypothyroidism; cholesterol ester storage disease;
KW
immune deficiency; immune disorder; infectious disease;
KW
autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW
myasthenia gravis; Gene; ss.

XX
OS
Homo sapiens.

XX
XX
FN
WO200192523-A2.

XX
XX
PD
06-DEC-2001.

XX
XX
PF
29-MAY-2001; 2001WO-US010836.

XX
XX
PR
30-MAY-2000; 2000US-0206132P.

XX
XX
PR
29-AUG-2000; 2000US-0228716P.

XX
XX
PA
(CURA-) CURAGEN CORP.

XX
XX
PI
Shimkets RA, Leach MD;

XX
XX
DR
WPI; 2002-106308/14.

XX
XX
DR
P-PSDB; ABP00589.

XX
PT
Novel human polypeptides and polynucleotides useful for diagnosing,
PT
preventing and treating cardiovascular disease, neurodegenerative,
PT
hyperproliferative disorders and autoimmune disorders.

XX
PS
Disclosure; SEQ ID NO 1159; 1037pp; English.

XX
CC
The present invention describes substantially purified human proteins
CC
(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC
in the specification). ABN15762 to ABN27252 encode the human ORFX
CC
proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC
treating or preventing a pathology associated with an ORFX-associated
CC
disorder in humans, and in the manufacture of a medicament for treating a
CC
syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC
sequences can be used in gene therapy. ORFX sequences can be used in the
CC
treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC
psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC
osteoarthritis, neurodegenerative disorders, disorders related to organ
CC
transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC
lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC
storage disease, various immune deficiencies and disorders, infectious
CC
diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC
arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC
disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC
useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC
bone degenerative disorders, or periodontal disease, and for gut
CC
protection or regeneration and treatment of lung or liver fibrosis,
CC
reperfusion injury in various tissues and conditions resulting from
CC
systemic cytokine damage. N.B. The sequence data for this patent did not
CC
form part of the printed specification, but was obtained in electronic
CC
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ
Sequence 257 BP; 53 A; 65 C; 99 G; 40 T; 0 U; 0 Other;

Query Match

6.5%; Score 32.6; DB 6; Length 257;

Best Local Similarity 57.3%; Pred. NO. 3.5;

Matches 59; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 206 TTAGTCGGGTTTAACGGTTGCCAGCGAGTGGTGGACCAAGACGCTAGTCTGGGAGCG 265
DB 110 TCATTCCGGGTTTCAACGGAGCCCGGACCTGGTGCAAAAGGACGTGCCAGGAGGC 169
QY 266 AAACCATATTGAGTCATCTTGGCAGAGCATGCACAATTCTGCA 308
DB 170 CAAAGGTGCGGTGAGCCCTGCATAGCCCCCACTAGATGCA 212

Search completed: August 4, 2004, 12:06:56
Job time : 307 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 11:56:01 ; Search time 63 Seconds
(without alignments)
4404.372 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcggc.....atcaggaaatgggatcgaaa 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	36.4	7.3	1263	4	US-09-107-532A-352
C 2	34.8	7.0	152331	3	US-09-128-155-16
C 3	33.4	6.7	468	4	US-09-252-991A-15459
C 4	33.4	6.7	1014	4	US-09-252-991A-15280
C 5	33.4	6.7	1842	4	US-09-252-991A-15508
C 6	32.4	6.5	831	4	US-09-489-039A-2499
C 7	31.2	6.2	732	4	US-09-134-000C-348
C 8	31	6.2	1825	4	US-09-976-594-673
C 9	31	6.2	2163	4	US-09-134-000C-2226
C 10	31	6.2	2640	4	US-08-684-932A-37
C 11	31	6.2	2655	4	US-09-016-434-1094
C 12	31	6.2	2655	4	US-09-023-655-916
C 13	30.6	6.1	392000	4	US-10-027-983-11
C 14	30.4	6.1	5722	4	US-09-566-921-54
C 15	30	6.0	426	3	US-09-441-346A-3
C 16	30	6.0	426	4	US-09-789-453A-3
C 17	30	6.0	455	4	US-09-621-976-10754
C 18	30	6.0	2847	4	US-09-484-970B-22
C 19	29.8	6.0	162	4	US-09-017-754A-6
C 20	29.8	6.0	255	4	US-09-516-667-85
C 21	29.6	5.9	921	4	US-09-489-039A-6123
C 22	29.6	5.9	17846	4	US-08-956-171E-109
C 23	29.4	5.9	7218	1	US-08-232-463-14
C 24	29.4	5.9	1830121	4	US-09-557-884-1
C 25	29.4	5.9	1830121	4	US-09-643-990A-1
C 26	29.2	5.8	1158	4	US-09-545-569A-9
C 27	29.2	5.8	1164	4	US-09-545-569A-1

28 29.2 5.8 1164 4 US-09-545-569A-2 Sequence 2, Appli
29 29.2 5.8 1164 4 US-09-545-569A-3 Sequence 3, Appli
30 29.2 5.8 1164 4 US-09-545-569A-5 Sequence 5, Appli
31 29.2 5.8 1164 4 US-09-545-569A-7 Sequence 7, Appli
32 29.2 5.8 1805 1 US-08-112-630-1 Sequence 1, Appli
33 29.2 5.8 3967 4 US-09-672-749-14 Sequence 14, Appli
34 29.2 5.8 129908 4 US-09-585-858-1 Sequence 1, Appli
35 29.2 5.8 193303 4 US-09-497-855A-37 Sequence 37, Appli
36 29.2 5.8 193303 4 US-09-497-855A-44 Sequence 44, Appli
37 29 5.8 500 3 US-09-141-000-2 Sequence 2, Appli
38 29 5.8 3048 1 US-07-921-807B-1 Sequence 1, Appli
39 29 5.8 3048 1 US-08-441-944A-1 Sequence 1, Appli
40 29 5.8 40328 3 US-08-742-185-102 Sequence 102, App
41 29 5.8 319608 4 US-09-539-333D-1 Sequence 1, Appli
42 29 5.8 319608 4 US-09-679-409-1 Sequence 2, Appli
43 29 5.8 4403765 3 US-09-103-840A-2 Sequence 1, Appli
44 29 5.8 4411529 3 US-09-103-840A-1 Sequence 1, Appli
45 28.8 5.8 534 4 US-09-252-991A-11597 Sequence 11597, A

ALIGNMENTS

RESULT 1
US-09-107-532A-352/c
; Sequence 352, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 352:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1263 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1263

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; SEQUENCE DESCRIPTION: SEQ ID NO: 352:
US-09-107-532A-352

Query Match
Best Local Similarity 7.3%; Score 36.4; DB 4; Length 1263;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 292 GCATGCACATCTCGAGGCGCATAGATTGTTTTCGATTTTACATGTGATTTTCA 351
Db 293 GCAATCACTAATCGATGATCAGTTGTTTTCGATTTTTCGATTTTCA 234
QY 352 ACAAAAATAACACTTGTCTCTGACACATATTTTCGACATATTCGGGCGATATTTAAAGTGT 411
Db 233 CTAATCAAAACAAAATAGTGACCAATAAAGAGGAGGAGCAGTCGTTAATAATTCACAGCA 174
QY 412 AACAAAGGAATCCGGGCAAG 433
Db 173 GATAAAGAACGCGTGGCATAAG 152

RESULT 2
US-09-128-155-16
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER FILING DATE: 1998-07-02
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match
Best Local Similarity 7.0%; Score 34.8; DB 3; Length 152331;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 280 CATCTTGGCAGCATGCACATTTCTGAGGCGCATAGATTGTTTTCGATTTTACAT 339
Db 66513 CAGCAGGAAAAGTATATACATTTTCAAAAGAAATAATACATTTCTGTCAGTTTCTTAC 66572
QY 340 GTGATTTTTCACAAAATAACACTTGTCTGACACATATTTTCGACATATTCGGGCAAT 399
Db 66573 ATATATTTTAAAGTAATAATCAATGTTAGGAAACATTTTAAATATGCCAACCTC 66632
QY 400 AATTAAGGTGTAAACAGGAA 421
Db 66633 ATTAATAATTATAGAGTGAAA 66654

RESULT 3
US-09-252-991A-15459
; Sequence 15459, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136

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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15459
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15459

Query Match
Best Local Similarity 6.7%; Score 33.4; DB 4; Length 468;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 83 CTCGGATAAGCCAGCGCCCATATTTTCAGGAGGATTCGCTCGGTTTGGCGACATTC 142
Db 220 CGCGGACTACGCTGTACCCCGAGGTTTGGCCGGAAGCGAGCGCGGCGTCTCGA 279
QY 143 GGATCCCGGAACCAAGCTCTGCAATGACCTGCGCGCCGAGGAAAGCGAGTGGTGCGAG 202
Db 280 GGCTTCGCTGACATGACGCTCTATCGCGCGCGCGGAGAGCGCGGCGTCTCGA 339
QY 203 GTTTTATGTCGGGTTTAAAGCTTCCAGGCGAGTGGTTCAGCAAGACGCTAGTCTGGGG 261
Db 340 GCTGCGGTGGGGTTGCTGTGCTCCATGCGGAGGCGTGCACTTTCTCCAGTGGCGG 398

RESULT 4
US-09-252-991A-15280/c
; Sequence 15280, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15280
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15280

Query Match
Best Local Similarity 6.7%; Score 33.4; DB 4; Length 1014;
Matches 88; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 83 CTCGGATAAGCCAGCGCCCATATTTTCAGGAGGATTCGCTCGGTTTGGCGACATTC 142
Db 842 CGCGGACTACGCTGTACCCCGAGGTTTGGCCGGAAGCGAGCGCGGCGGAGTCTCT 783
QY 143 GGATCCCGGAACCAAGCTCTGCAATGACCTGCGCGCCGAGGAAAGCGAGTGGTGCGAG 202
Db 782 GGCTTCGCTGAAACATGACGCTCTATCGCGCGCGCGGAGGAGCGCGGCGTCTCGA 723
QY 203 GTTTTATGTCGGGTTTAAAGCTTTCAGGCGAGTGGTTCAGCAAGACGCTAGTCTGGGG 261
Db 722 GCTGCGGTGGGGTTGCTGTGCTCCATGCGGAGGCGTGCACTTTCTCCAGTGGCGG 664

RESULT 5
US-09-252-991A-15508
; Sequence 15508, Application US/09252991A
; Patent No. 6551795

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RESULT 7

RESULT 9

US-09-134-000C-2226
; Sequence 2226, Application US/09134000C
; Patent No. 6617156
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58...2523
; US-08-684-932A-37
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58...2523
; US-08-684-932A-37
Query Match 6.2%; Score 31; DB 4; Length 2163;
Best Local Similarity 64.8%; Pred. No. 2.8;
Matches 46; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2226
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2226

Query Match 6.2%; Score 31; DB 4; Length 2163;
Best Local Similarity 64.8%; Pred. No. 2.8;
Matches 46; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 310 GGCATAGATTGGTTTGGCTCGCATTTACAAATGATTTTTCACAAAATAACACTGGT 369
DB 859 GGGATATATTTTGGTTTAAATGTTAACTATTCTATTACTGACAATAATGCTCTGTT 918
QY 370 CTGACCACATT 380
DB 919 CTAATCTCTTT 929

RESULT 10

US-08-684-932A-37/c
; Sequence 37, Application US/08684932A
; Patent No. 6403304
; GENERAL INFORMATION:
; APPLICANT: Stashenko, Philip
; APPLICANT: Li, Yi-Ping
; TITLE OF INVENTION: HUMAN OSTEOCLAST-SPECIFIC AND -RELATED
; TITLE OF INVENTION: DNA SEQUENCES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,932A
; FILING DATE: 19-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: FDC92-02FM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2640 base pairs
; TYPE: nucleic acid

US-09-016-434-1094/c
; Sequence 1094, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1094:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1245045
US-09-016-434-1094

RESULT 11

US-09-016-434-1094/c
; Sequence 1094, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1094:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1245045
US-09-016-434-1094


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; LOCATION: (220360)...(220459)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (222717)...(222816)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (223981)...(224080)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (227487)...(227586)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (230157)...(230256)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (232259)...(232398)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (236552)...(2366651)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc feature
; LOCATION: (238789)...(248788)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: exon
; LOCATION: (118288)...(119101)
; OTHER INFORMATION: exon 1C
; NAME/KEY: exon:intron junction
; LOCATION: (151129)...(151130)
; OTHER INFORMATION: exon 5:intron 5
; NAME/KEY: exon:intron junction
; LOCATION: (299248)...(299249)
; OTHER INFORMATION: exon 9:intron 9
; NAME/KEY: exon:intron junction
; LOCATION: (348578)...(348579)
; OTHER INFORMATION: exon 10:intron 10
; NAME/KEY: intron
; LOCATION: (348579)...(381838)
; OTHER INFORMATION: intron 10
; NAME/KEY: intron:exon junction
; LOCATION: (386185)...(386186)
; OTHER INFORMATION: intron 11:exon 12
; US-10-027-983-11
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Query Match          6.1%; Score 30.6; DB 4; Length 392000;
Best Local Similarity 49.7%; Pred. No. 64;
Matches 78; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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QY 266 AAACATATTGAGTCATCTTGCGAGCATGCACAAATCTGCGAGGCATAGATTGGTTT 325
DB 253273 AACCTAAAGCAATCATTTAGCCAAAAGGGGAGATGGGTAGGGGAAAGATGAAAA 253214

QY 326 GCTCGATTTACAATGTGATTTTTCACAAAATAACACTGGTCTGACCAATTTTCGG 385
DB 253213 GAAGGGTAAATGTACAAATATTTCATCTCATCAAGTCACCAATAGATATGTCCA 253154

QY 386 ACATAATCGGCATAAATTAAGGTCTAACAAAGGAAT 422
DB 253153 AGTTGATAAGTCAAAATATAGGTTTATTATAGGTAT 253117
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RESULT 14
US-09-566-921-54
; Sequence 54, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
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; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 5722
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inceyte ID No. 6682888 331485.3
US-09-566-921-54
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Query Match          6.1%; Score 30.4; DB 4; Length 5722;
Best Local Similarity 61.2%; Pred. No. 7.6;
Matches 49; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 294 ATGCACAATTCGACGGCATAGATTGGTTTCTCGATTTCACATGTGATTTTCAAC 353
DB 2472 ATGTAGATTTAGGATGCCCTATTGCTGCTTTCTAGATTAAATGAGATCTTTGAACC 2531

QY 354 AAAAATPACACTTGGTCTGA 373
DB 2532 AGGAGGAGATCTTCATCTGA 2551
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RESULT 15

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US-09-441-346A-3
; Sequence 3, Application US/09441346A
; Patent No. 6242588
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Fiddington, Christopher S.
; APPLICANT: Ellsworth, Jeff L.
; TITLE OF INVENTION: TESTIS-SPECIFIC GLYCOPROTEIN ZPEP10
; FILE REFERENCE: 98-34
; CURRENT APPLICATION NUMBER: US/09/441,346A
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,216
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zpep10
; OTHER INFORMATION: polypeptide of SEQ ID NO:2
; NAME/KEY: variation
; LOCATION: (1)....(426)
; OTHER INFORMATION: Each N is independently any nucleotide.
US-09-441-346A-3
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Query Match          6.0%; Score 30; DB 3; Length 426;
Best Local Similarity 25.8%; Pred. No. 2.5;
Matches 51; Conservative 37; Mismatches 110; Indels 0; Gaps 0;

QY 6 AGCCAGGTAGCGGTGTACACCCACCGTTTCGGCAACAATGACGGCGAGAGAGCCCA 65
DB 88 MGNVTGNCNMGNNTNTGYWSNCARATGGARCNMGNCARARGARTGYGNGCWNSCN 147

QY 66 CCACATTGCGATTTCCGCTCCGATTAAGCCAGCCCATATTTGCAGGAGGATTCGCT 125
DB 148 GAYTTYWSNGCNTTYGCTNYNGAYGARGTNWSNATGAAYARGTNACNGARARACNCAY 207

QY 126 GCGGTTTGGCGACATTCGGATCCCGGAAACCAGCTCTGCAATGACCTCGCGCGGAGGA 185
DB 208 MGNGTNTNMGNGTATGGNGGWSNACNACNTTNTAYAYTGYWSNACNTGYAARGGN 267

QY 186 AGCCAGGTGGGTGGCAGG 203
DB 268 ACNGARGTNWSNTGYTGG 285
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Search completed: August 4, 2004, 13:25:24

us-09-987-763-7.rni

Fri Aug 6 10:32:28 2004

Job time : 71 secs

Fri Aug 6 10:32:29 2004

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 11:50:56 ; Search time 2380 Seconds

(without alignments)
6273.567 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgcc.....atcaggaaagtggaatcgaaa 500

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_estum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.4	8.5	1018	12	BG684402
C 2	41.2	8.2	1201	13	BX394291
C 3	40.0	8.0	1610	28	AF057117
C 4	38.6	7.7	1201	13	BX381961
C 1	42.4	8.5	1018	12	BG684402
C 2	41.2	8.2	1201	13	BX394291
C 3	40.0	8.0	1610	28	AF057117
C 4	38.6	7.7	1201	13	BX381961

C 5	7.6	743	28	BZ146910
C 6	7.6	1221	29	AG058113
C 7	7.6	835	14	CK203550
C 8	7.4	682	28	AZ420591
C 9	7.3	1201	9	AL519510
C 10	7.3	1215	28	CC285387
C 11	7.3	570	28	BH428607
C 12	7.3	672	28	AG167527
C 13	7.3	725	28	BZ514039
C 14	7.3	732	28	BZ453110
C 15	7.3	837	28	AZ129743
C 16	7.2	885	13	BX425603
C 17	7.2	417	13	BY637673
C 18	7.2	456	9	AI722358
C 19	7.2	755	28	BZ061578
C 20	7.2	1201	13	BX376774
C 21	7.1	1201	13	BX340397
C 22	7.1	685	29	AG183454
C 23	7.0	1252	28	CC324229
C 24	7.0	635	29	CE015870
C 25	7.0	345	10	BF714393
C 26	7.0	559	28	AQ061172
C 27	7.0	663	9	AV972628
C 28	7.0	916	29	CNS04E41
C 29	7.0	1029	29	CNS016QV
C 30	7.0	1201	13	BX416614
C 31	6.9	674	13	BW010388
C 32	6.9	748	28	BZ341132
C 33	6.9	893	14	CK245533
C 34	6.9	1201	13	BX353189
C 35	6.9	331	10	BF231100
C 36	6.9	524	12	BG097296
C 37	6.9	1201	13	BX399745
C 38	6.9	1201	13	BX419736
C 39	6.8	237	10	BB007989
C 40	6.8	338	10	BB519478
C 41	6.8	555	14	CA276805
C 42	6.8	565	13	BQ018827
C 43	6.8	605	13	BQ857538
C 44	6.8	684	29	AG095157
C 45	6.8	1101	29	CNS00F1J

ALIGNMENTS

RESULT 1

BG684402/c

LOCUS

DEFINITION

602636153F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4763989 5',

mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1018 bp mRNA linear EST 01-MAY-2001
BG684402 602636153F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4763989 5',
mRNA sequence.

ACCESSION BG684402

VERSION BG584402.1 GI:13915799

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1018)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1620 row: i column: 14

High quality sequence stop: 4.

FEATURES

Location/Qualifiers

1. .1018
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4763989"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_48"
 /notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 8.5%; Score 42.4; DB 12; Length 1018;
 Best Local Similarity 57.6%; Pred. No. 0.15; Indels 0; Gaps 0;
 Matches 76; Conservative 0; Mismatches 56;
 QY 61 GCCACCATTCGCGATTCGCTCCGATAAAGCCAGCGCCCATATTTTCAGGAGGATT 120
 DB 153 GGCAACCTGATGGAGACTCTTCTCGATAGGCAAGTCAAGTGGAGTGGTC 94
 QY 121 CGCTCGGTTGGGACATTCGGATCCCGGACCAACAGCTCTGCAATGACCTCGCGCGCG 180
 DB 93 ATGCGTCGATTGCTCACAATCGGCACCTGGGAGCCAGAGCAGCATGGAGCCCCATGGAG 34
 QY 181 AGGGAAGCGAGG 192
 DB 33 CTGCAAGCGAGG 22

RESULT 2

BX394291 1201 bp mRNA linear EST 13-MAY-2003
 LOCUS BX394291 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION cDNA clone CS0DC013YA05 3-PRIME, mRNA sequence.
 ACCESSION BX394291
 VERSION BX394291.1 GI:30628159
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0DC013YA03NP1.
 Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC013YA05"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

Location/Qualifiers

1. .1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DC013YA05"
 /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 8.0%; Score 40; DB 28; Length 1610;
 Best Local Similarity 48.3%; Pred. No. 0.96;

ORIGIN

Query Match 8.2%; Score 41.2; DB 13; Length 1201;
 Best Local Similarity 12.6%; Pred. No. 0.37; Indels 0; Gaps 0;
 Matches 49; Conservative 166; Mismatches 174;
 QY 112 GGGAGGATTCGCTGGGGTTTGGCGATTCGGATCCCGAACCAGCTCTGCAATGACC 171
 DB 596 KKKKKKKKCAABCKGKKKKKAAADKKKKYBKCANCAAYCAKKKADKKKKCK 655
 QY 172 TGGCGCCGCGGAGGAGGAGGTTGGGAGGTTTGTAGTCGGGTTTAAAGCTTGCAGG 231
 DB 656 KKCCDNAMCCMBECNCCCKKCNKBCCKCTCKBKAAMKKCKTCKBMMKKAAB 715
 QY 232 CGAGTGTGTGAGCAACAGCTAGTCTGGGAGCGAACCATATTTAGTCACTCTGGCAG 291
 DB 716 KKKAKKAAKAAABCAKADKABNKKRKBKBAAMNCAADAKKKKBKAKKKSKS 775
 QY 292 GCATGCACAAATTCGAGGGCATAGATTTGCTCGATTTTACAAATGTGATTTTCA 351
 DB 776 AMAHBKCAAMTTTKAMABAAATHBCMTTKMTTMMCTHTKCTKKNKVMKKKKKK 835
 QY 352 ACAGAAATTAACACTTGGTCTGACCATTTTCGGACATTAATCGGCGATTAATAAGGT 411
 DB 836 MHBACAMTKKWTNKTCKKGMKTMCMCKKKKKKANKAMKKKKKKKAMMAHMAAMK 895
 QY 412 AACAAAGGAATCCGGSCAAGCTCTTGCTGATTTTCTGAGCTGCTTTTGGGTTGTCG 471
 DB 896 CMKKKKMKKKKKKKKAMMMCKKKKKKKKKKKKAMMMKMMKMMKMMKMMKMMKMM 955
 QY 472 GTTAGGAAATCAGGAAGTGGGATCGAAA 500
 DB 956 MAAWKAAHAAACMNCCKAKKKKKKKA 984

RESULT 3

AF057117 1610 bp DNA linear GSS 21-FEB-2001
 LOCUS AF057117 Human Homo sapiens genomic clone 016H probe, genomic
 DEFINITION survey sequence.
 ACCESSION AF057117
 VERSION AF057117.1 GI:3142424
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1610)
 Janer, M. and Geraghty, D.E.
 The human major histocompatibility complex: 42,221 bp of genomic
 sequence, high-density sequence-tagged site map, evolution, and
 polymorphism for HLA class I
 Genomics 51 (1), 35-44 (1998)
 JOURNAL 98360090
 MEDLINE 98360090
 PUBMED 98360090
 COMMENT Contact: Janer M
 Geraghty Lab
 Fred Hutchinson Cancer Research Center
 1100 Fairview Ave., D2-100, Seattle, WA 98109-1024, USA
 Email: geraghty@fhcr.org
 Class: unknown.
 Location/Qualifiers
 1. .1610
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="p21.3; HLA Class I region"
 /clone="016H probe"
 /clone_lib="Human"

FEATURES

Location/Qualifiers
 1. .1610
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="p21.3; HLA Class I region"
 /clone="016H probe"
 /clone_lib="Human"

ORIGIN

Query Match 8.0%; Score 40; DB 28; Length 1610;
 Best Local Similarity 48.3%; Pred. No. 0.96;

Matches	112;	Conservative	0;	Mismatches	120;	Indels	0;	Gaps	0;
QY	47	ATGACGGCGAGAGAGCCACCA	CATTGGCGATTTCGCTCCGATAAGCAGCGCCATAT	106					
Db	538	AGGCGGCGGACAGCGCCCA	CCGCGGAGAGGGGCTGCCAAAAGGCAAGCAGCATAG	597					
QY	107	TTGACGGAGGANTCGCTCGGTTGGTGACATTCGATCCCGGAAACCACTCTGCAA	166						
Db	598	GAGATGACGAGGGGTGCTGCTGCTCGGAGACTCATCTCCCAACCCACCGATGCCA	657						
QY	167	TGACTCGCGCCCGAGGAGACGAGTGGTGCGAGGTTTATGTGCGGTTTAAAGGTTG	226						
Db	658	CAAGGTAGAGCGCGAGACAGCGAGGTGCGCGGATTCGCGACCCCTGCTCCCAACC	717						
QY	227	CCAGCGGAGTGGTGAGCAAGACGCTAGTCTGGGGAGCGAAACCATATTGAG	278						
Db	718	GCCCATGCGGGGAGAGACTACCGCGCGCAAGCAGAACGACGACGAG	769						
RESULT 4									
LOCUS	BX3811961/c								
DEFINITION	clone CS0DI072YF05 3-PRIME, mRNA sequence.								
ACCESSION	BX3811961								
VERSION	1								
KEYWORDS	EST.								
SOURCE	Human								
ORGANISM	Homo sapiens (human)								
REFERENCE	1 (bases 1 to 1201)								
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.								
TITLE	Full-length cDNA libraries and normalization								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Genoscope								
FEATURES	Genoscope - Centre National de Sequencage								
source	BP 191 91066 EVRY cedex - France								
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr								
	Library was constructed by life technologies, a division of								
	Invitrogen. Contact : Feng liang Email : fliang@lifetech.com URL :								
	http://fulllength.invitrogen.com/Invitrogen Corporation 1600								
	Paradise Avenue Genoscope sequence ID : CS0DI072C03NPL.								
	Location/Qualifiers								
	1. .1201								
	/organism="Homo sapiens"								
	/mol_type="mRNA"								
	/db_xref="taxon:9606"								
	/clone="CS0DI072YF05"								
	/tissue_type="PLACENTA COT 25-NORMALIZED"								
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"								
	/note="1st strand cDNA was primed with a NotI-oligo (dT)								
	primer. Five prime end enriched, double-strand cDNA was								
	digested with NotI and cloned into the NotI and EcoRV								
	sites of the pCMVSPORT 6 vector. Library was normalized."								
ORIGIN									
Query Match	7.7%; Score 38.6; DB 13; Length 1201;								
Best Local Similarity	8.9%; Pred.No.2.3;								
Matches	31; Conservative 177; Mismatches 141; Indels 1; Gaps 1;								
QY	85	CCGATAAAGCCAGCCCATATTTCAGGAGGAGATTCCCTCGGGTTTGGCAGCATTCGG	144						
Db	1138	MMGBBMMVGVGKGGKGGKGMVMMGGCMSCVKKGNSKGCBCGCKGCGKCGCMK	1079						
QY	145	ATCCCCGGAAACAGAGCTCTCAATGACCTCGCGCGGAGGAGCGAGTGGTGGGAGC	204						
Db	1078	GKVVXGMBMMKKKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM	1020						
QY	205	TTTAGTGGCGGTTTAAAGCGTTCCAGCGGAGTGGTGAGCAAGACGCTAGTCTGGG	264						
Db	1019	BMKTGKKKKKGGMMGMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMMKMM	960						

Db 481 AATTCATGACATATTCGTAGCACTCTCTGTGTGTAACACACTCAGAAAAACAACACT 422
 QY 438 TGCTGATTTCTGAGCTGCTTTGTGGTGTGTCGGTTA 475
 Db 421 GTAGAAGTTAGTCTACTGCTCTTTCTTTGTGTCTAGTTA 384

RESULT 6
 AG058113
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: PTB-044012.F, genomic survey sequence.
 AG058113
 VERSION AG058113.1 GI:16595574
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of Library PTB
 Unpublished
 2 (bases 1 to 1221)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpbes@sc.riken.go.jp, URL: http://bgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB. This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: -21M13
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..1221
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-044012.F"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES

source

ORIGIN

Query Match 7.6%; Score 38; DB 29; Length 1221;
 Best Local Similarity 49.2%; Pred. No. 3.6;
 Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 QY 49 GACGCGGAGAGAGCCACCATTCGATTCCTCGATTAAGCCAGCGCCCATATTT 108
 Db 874 GCCCGGAGGAGGCCCGCCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 933
 QY 109 GCAGGAGGATTCGCTGCGGTTTGGCGACATTCGATCCCGGAGACGCTCTGCAATG 168
 Db 934 GCGCGGCG 993
 QY 169 ACCTGCG 228
 Db 994 GCG 228
 QY 229 AGCGGAGTGTGAGCAAAAG 247
 Db 1054 GCG 1072

RESULT 7

CK203550

LOCUS

DEFINITION

CK203550

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooideae; Triticeae; Triticum.
 1 (bases 1 to 835)
 Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroché, A.,
 Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
 Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress in Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada
 Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_est@cs.usask.ca
 This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [102,729].
 Plate: L3C117 row: C column: 10.

FEATURES

source

1..835

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
 control, cold-acclimated and salt stressed wheat cultivar
 Norstar. 7 mRNA populations were combined before
 constructing the library; 7 day non-acclimated roots, 1,
 23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
 hours and 6 hours treated roots with 200mM NaCl.
 Non-acclimated and cold-acclimated plants were grown in
 vermiculite while salt stressed plants were grown
 hydroponically. First strand synthesis in this library was
 done in the presence of methylated dCtp thereby protecting
 from internal cleavage with NotI."

ORIGIN

Query Match 7.6%; Score 37.8; DB 14; Length 835;
 Best Local Similarity 57.0%; Pred. No. 3.6;
 Matches 69; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 QY 339 TGTGATTTTTCACAAAATAACACTTGGTCTGACCACTTTTCGACATAATCGGCA 398
 Db 445 TGTTGGTTATTCAAGAGATCAACTTCTTGACCTGGCAAGATTACTGATGTAACCGACA 504
 QY 399 TAATTAAGGTGTAAACAAGGAATCCGGGCAACAGCTTCTGCTGATTTTCTGAGCTGTT 458
 Db 505 AATCTGAGGCTTCAGCAAGAAATTTGAAGCAGAGCTTCATGTCAGCATCAGAGCTGGT 564
 QY 459 T 459
 Db 565 T 565

RESULT 8

AZ420591/c

LOCUS AZ420591 682 bp DNA linear GSS 03-OCT-2000
 DEFINITION 1M0198D05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0198D05 R, genomic survey sequence.
 ACCESSION AZ420591
 VERSION AZ420591.1 GI:10544604
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 682)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0198 row: D column: 05
 Seq primer: CACAGGAAACAGTATGACC
 Class: plasmid ends
 High quality sequence stop: 682.
 Location/Qualifiers
 1. 682
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0198D05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: FWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pW42 (G114732114[gb]AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 7.4%; Score 36.8; DB 28; Length 682;
 Best Local Similarity 55.5%; Pred. No. 6.9;
 Matches 71; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 289 AGAGCATGCACAAATCTCGAGGCGCATAGATTGGTTTCTCGATTACAAATCTGATTTT 348
 DB 630 AGAGCTTGTGGTCTTCAAGATATGATTTTCAATTTGGCCCAATAAAAAATGTTTAT 571
 QY 349 TCAACAAAAATACACTTGGTCTGACCACATTTTCGGACATATCGGGCATATTAATTAAGG 408
 DB 570 TTATAAAGATATTCATAGATTGGCTTAGATTGAGCCGCGCATCTCTAGAAATTAACA 511

QY 409 TGTACAA 416
 DB 510 CATGAAGA 503
 RESULT 9
 AL519510 1201 bp mRNA linear EST 22-MAY-2003
 LOCUS AL519510
 DEFINITION AL519510 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 cDNA clone CSODB004YA16 5-PRIME, mRNA sequence.
 ACCESSION AL519510
 VERSION AL519510.2 GI:31037857
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1201)
 Li,W.B., Gruber,C., Tessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 13, 2001 this sequence version replaced gi:12783003.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 781.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSODB004BA08QPI&cluster=781.f. Contact :
 Feng liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CSODB004BA08QPI.
 Location/Qualifiers
 1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODB004YA16"
 /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 7.3%; Score 36.6; DB 9; Length 1201;
 Best Local Similarity 27.7%; Pred. No. 9.7;
 Matches 74; Conservative 74; Mismatches 118; Indels 1; Gaps 1;
 QY 11 GGTAGCGGCTTAACCCACACCGTTCGGCAACATGACGCGGAGAGCCACCA 70
 DB 544 SSSSTSSSTATASATSTSSAGSATSTSSASATSTSSSSSTSTSSSSASSTSA 603
 QY 71 TTGCGATTCCGTCGATTAAGCCAGCCGCCATATTG-CAGGAGGATTGCGTCGG 129
 DB 604 SASASSSTSTSTSTSTTASATSSSSSSATSTSSSSSTSTSSSTSSASSTSS 663
 QY 130 TTGGCGCATTCGGATCCCGAACACGCTCTCAATGACCTCGCGGCCGAGGAACG 189
 DB 664 SSSSTSSSSSSAGTSTSSASSASSASITSTSSASSAATSTSTSSGAGATGAGG 723
 QY 190 AGTGGTGGCGCAGGTTTGTAGTCGGGTTTAAAGCTTCCAGCGGAGTGTGAGCAAGAC 249
 DB 724 ATGTGAGGCTGATCGGSAGTGGTGTGGATGGAGGAGTGGGAGTGGAGGGTG 783
 QY 250 GCTAGTCTGGGAGCGAAACCATATTG 276
 DB 784 GATAGTGGAGGGGGTGAAGAAGATTG 810

FEATURES
 source

```

RESULT 10
CC285387/c
LOCUS
DEFINITION
  CC285387
  1215 bp DNA linear GSS 13-MAY-2003
  genomic survey sequence.
ACCESSION
  CC285387
VERSION
  CC285387.1 GI:30653842
KEYWORDS
  GSS.
SOURCE
  Gallus gallus (chicken)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
REFERENCE
  1 (bases 1 to 1215)
  Krenitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
  Warren, W., Graves, T., Mardis, E. and Wilson, R.
  Gallus gallus BAC End Reads
  Unpublished (2003)
  Contact: Richard K. Wilson
  Genome Sequencing Center
  Washington University School of Medicine
  Email: submissions@watson.wustl.edu
  Insert Length: 182000 Std Error: 0.00
  Seq primer: Sp6 ATTGAGTGACACTATAG
  Class: BAC ends
  High quality sequence start: 195
  High quality sequence stop: 386.
  Location/Qualifiers
    1..1215
    /organism="Gallus gallus"
    /mol_type="genomic DNA"
    /strain="Red Jungle Fowl"
    /db_xref="taxon:9031"
    /clone="CH261-28H5"
    /sex="female"
    /cell_line="UCD001, inbred 256"
    /clone_lib="CH261"
    /notes="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
    CH261 Female Chicken library - for library and clone
    ordering information: http://www.chori.org/bacpac"
ORIGIN
  Query Match 7.3%; Score 36.6; DB 28; Length 1215;
  Best Local Similarity 52.3%; Pred. No. 9.7;
  Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
  QY 331 ATTCAATGCTGATTTTTCACAAATAATACACTGGCTGACACATTTTCGGACATA 390
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 318 ATTGACAGTTTATTTTAAACAAAGAAAGATAGAAATACTTCTGTTTCAATTA 259
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  QY 391 ATCGGGCATAATTAAGGTGTAACAAAGGAATCCGGGCACAGCTTCTGCTGATTTCTG 450
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 258 TTCTCAGAACATTCAGCGGTAAAGAAATCAATGACAGATGTTGAGGGCTTGCTTTA 199
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  QY 451 AGCTGCTTTGCGTTGTCGGTTAGGGAATCAG 485
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 198 TTTTGCTATTGTTGTTGAAGGAAGGGAAGACAG 164
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
BH428607
LOCUS
DEFINITION
  BH428607
  570 bp DNA linear GSS 12-DEC-2001
  BOHS48TF BOHS Brassica oleracea genomic clone BOHS48, genomic
  survey sequence.
ACCESSION
  BH428607
VERSION
  BH428607.1 GI:17614328
KEYWORDS
  GSS.
SOURCE
  Brassica oleracea
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; eutrosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
  1 (bases 1 to 570)
  Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
  Whole genome shotgun sequencing of Brassica oleracea
  Unpublished (2001)
  Other GSSs: BOHSE48TR
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: cdtown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TF
  Class: sheared ends.
  Location/Qualifiers
    1..570
    /organism="Brassica oleracea"
    /mol_type="genomic DNA"
    /strain="TO1000DH3"
    /db_xref="taxon:3712"
    /clone="BOHSE48"
    /clone_lib="BOHS"
    /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
    genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN
  Query Match 7.3%; Score 36.4; DB 28; Length 570;
  Best Local Similarity 56.8%; Pred. No. 8.6;
  Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
  QY 233 GAGTGGTGACAAAGACGCTAGTCTGGGAGCGGAACCATATTGAGTCATCTTGGCAGAG 292
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 282 GAGAGCTGGGTTTAAGCAGAAAGCCTGTGGAGAGAGAGCTGTAGAGTCGTTAGGAGAA 341
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  QY 293 CATGCACAATTCGCGAGGCATAGATTGTTTTCGTCGATTTCACAAATGATTTTTC 350
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  Db 342 GATGAAGAGGTGGGGTTACCATTAAGACTTTGTGCTGTGAAGATAGTAATTGGTTTC 399
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
AG167527/c
LOCUS
DEFINITION
  AG167527
  672 bp DNA linear GSS 09-JAN-2002
  Pan troglodytes DNA, clone: RP43-035J24.T7, genomic survey
  sequence.
ACCESSION
  AG167527
VERSION
  AG167527.1 GI:16697205
KEYWORDS
  GSS.
SOURCE
  Pan troglodytes (chimpanzee)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
  1 (bases 1 to 672)
  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
  Totoki, Y., Watanabe, H. and Sakaki, Y.
  BAC end sequences of Library RPCI-43
  Unpublished
  2 (bases 1 to 672)
  Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
  Totoki, Y., Watanabe, H. and Sakaki, Y.
  Direct Submission
  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
  Tel: 81-45-503-9111, Fax: 81-45-503-9170)
  Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
  end was generated during the R&D process and may have higher chance
  of clone tracking errors.
  PRIMERS
  Sequencing: T7
  LIBRARY
  Vector : pBACe3.6
  R.Site 1 : EcoRI

```

R.Site 2 : EcoRI

Location/Qualifiers
1..672
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-035J24.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 7.3%; Score 36.4; DB 29; Length 672;
Best Local Similarity 52.7%; Pred. No. 9.1; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 71;

QY 322 TTTTGTCTGATTTACAATGGATTGTTTTTCACAAAATAAAGACTTGCTGCACCAATTT 381
|||||
Db 155 TTTCGGAGGATTAAATTTGGAGTTTGTAAAGAAAAAATTTAGATGGTTTCTTAATTTT 96
|||||
QY 382 TC GGACATATCCGGCATTAATTAAGGTGAACAAGGAATCCGGGCCAACAGCTCTTGCT 441
|||||
Db 95 TCTTAAAGGATCGGTCATCAGTTAAGGAATTTGAACCTACCACCGACACGTTTGA 36
|||||
QY 442 GATTTCTGAGCTGCTTTGTTGGTGTCTCGG 471
|||||
Db 35 GATCTTTAGAAAGAAGAACAGGGTTTCGGG 6
|||||

RESULT 13

BZ514039/c
LOCUS
DEFINITION
BZ514039 BO_2_3 KB Brassica oleracea genomic clone BOMQ266,
genomic survey sequence.
ACCESSION BZ514039.1 GI:27041484
VERSION BZ514039.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 725)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOMQ266TF
Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..725
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clones="BOMQ266"
/clone_lib="BO_2_3_KB"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 7.3%; Score 36.4; DB 28; Length 725;
Best Local Similarity 56.8%; Pred. No. 9.4; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 51;

QY 233 GAGTGGTAGCAACAGCGTAGTCTGGGGGCGGAAACCATATTGAGTCATCTTGGCAGAG 292
|||||
Db 398 GAGAGCTGGGTTTAAAGCAGAGCGCTGTGGAGAGAGAGCTTGTAGAGTCTTTAGGGAGAA 457
|||||
QY 293 CATGCACAATTTCTGCAGGGGCATAGATTGGTTTTTCATTTACATCTGATTTTTC 350
|||||
Db 458 GATGAAGAGGTGGGGTTACCATAAAGACTTTGTGCTTGTATGAAGATAGTAATTTGTTTC 515
|||||

RESULT 15

AZ129743/c
LOCUS
DEFINITION
AZ129743 OSJNB0068C15r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
cultivar-group) genomic clone OSJNB0068C15r, genomic survey
sequence.
ACCESSION AZ129743.1 GI:8207736
VERSION AZ129743.1
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
1. (bases 1 to 837)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 21
High quality sequence stop: 704.

FEATURES
Location/Qualifiers
1..837
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:3994"
/clone="OSJNB0068C15r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CGI Rice BAC Library (EcoRI)"
/note="Vector: pBACIndigo; Site 1: EcoRI; Site 2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9%. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

Source

ORIGIN

Query Match 7.3%; Score 36.4; DB 28; Length 837;
Best Local Similarity 53.5%; Pred. No. 9.8;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY	280	CATCTTGGCAGACGATGACAAATTCGAGGCGATAGATTTGGTTTCGATTTACAAAT	339
Db	582	CACATAGCCAAACCATTCAGTATATCCAGGACATAGTTTATCACAATAATTTTAAAT	523
QY	340	GTGATTTTTCACAAAAATAACACTTGGTCTGACCAATTTTCGGACATAATCGGGCAT	399
Db	522	AATATTAAATTTAAAAAAATTTTTCAGTTACCAATACACATAATAAATAATTCCTAAGT	463
QY	400	AATTAAAGGTGTAAACAAAGGAA	421
Db	462	AAATTAAGTAGTAGAAGGAA	441

Search completed: August 4, 2004, 13:23:57
Job time : 2385 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 12:44:02 ; Search time 318 Seconds
(without alignments)
7709.340 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagcaggttagcggc.....atcaggaagtggatcgaaa 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500	100.0	500	13	US-09-987-763-7
2	490.4	98.1	3309400	9	US-09-738-626-1
3	264	52.8	1776	13	US-09-738-626-3211
4	37.6	7.5	594	13	US-10-142-426-10
5	37.6	7.5	594	15	US-10-123-155-10
6	37.6	7.5	594	15	US-10-146-731-10
7	37.6	7.5	594	15	US-10-140-472-10
8	37.6	7.5	594	15	US-10-141-761-10
9	37.6	7.5	594	15	US-10-142-885-10
10	37.6	7.5	594	16	US-10-158-790-10
11	37.6	7.5	594	16	US-10-137-871-10
12	37.6	7.5	594	16	US-10-140-923-10
13	37.6	7.5	594	16	US-10-141-756-10
14	37.6	7.5	594	16	US-10-141-759-10

15	37.6	7.5	594	16	US-10-140-805-10	Sequence 10, Appl
16	37.6	7.5	594	16	US-10-140-864-10	Sequence 10, Appl
17	36.2	7.2	1053	13	US-10-282-122A-29887	Sequence 29887, A
18	34.8	7.0	1508	16	US-10-369-493-44140	Sequence 44140, A
19	34.8	7.0	152331	14	US-10-095-407-16	Sequence 16, Appl
20	34.2	6.8	32591	16	US-10-085-117-187	Sequence 187, App
21	34	6.8	433	13	US-10-424-599-4852	Sequence 4852, App
22	33	6.6	1328	13	US-10-027-632-123211	Sequence 123211, A
23	33	6.6	1328	16	US-10-027-632-123211	Sequence 123211, A
24	33	6.6	2278	13	US-10-424-599-117564	Sequence 117564, A
25	33	6.6	3563	17	US-10-437-963-47080	Sequence 47080, A
26	32.8	6.6	32191	10	US-09-764-891-8965	Sequence 8965, Ap
27	32.2	6.4	335	13	US-10-085-783A-4787	Sequence 4787, Ap
28	32.2	6.4	335	16	US-10-242-538A-4787	Sequence 4787, Ap
29	32.2	6.4	624	13	US-10-027-632-223801	Sequence 223801, A
30	32.2	6.4	624	16	US-10-027-632-223801	Sequence 223801, A
31	32.2	6.4	637	13	US-10-027-632-250227	Sequence 250227, A
32	32.2	6.4	637	16	US-10-027-632-250227	Sequence 250227, A
33	32.2	6.4	2632	15	US-10-198-846-11330	Sequence 11330, A
34	32.2	6.4	304905	13	US-10-271-416-1	Sequence 1, Appl
35	32	6.4	577	9	US-09-864-761-14811	Sequence 14811, A
36	32	6.4	701	13	US-10-027-632-236918	Sequence 236918, A
37	32	6.4	701	16	US-10-027-632-236918	Sequence 236918, A
38	32	6.4	701	16	US-10-027-632-236918	Sequence 236918, A
39	32	6.4	701	16	US-10-027-632-236918	Sequence 236918, A
40	32	6.4	796	17	US-10-437-963-40252	Sequence 40252, A
41	32	6.4	598	13	US-10-027-632-258465	Sequence 258465, A
42	32	6.4	598	16	US-10-027-632-258465	Sequence 258465, A
43	32	6.4	3186	13	US-10-027-632-114364	Sequence 114364, A
44	32	6.4	3186	16	US-10-027-632-114364	Sequence 114364, A
45	32	6.4	344548	13	US-10-087-192-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-09-987-763-7
; Sequence 7, Application US/09987763
; Publication No. US20030017553A1
; GENERAL INFORMATION:
; APPLICANT: Rayapati, P. John
; APPLICANT: Crafton, Corey M.
; TITLE OF INVENTION: Nucleotide Sequences for Transcriptional Regulation in Corynebacterium glutamicum
; TITLE OF INVENTION: Corynebacterium glutamicum
; FILE REFERENCE: 1533.1940002
; CURRENT APPLICATION NUMBER: US/09/987,763
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,219
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-987-763-7

Query Match	100.0%	Score	500;	DB	13;	Length	500;
Best Local Similarity	100.0%	Pred. No.	6.3e-157;				
Matches	500;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	AAAACAGCAGGTTAGCGGCTGTAAACCAACACCGGTTTCGGCAACAATGACGGGAGAGA	60				
Db	1	AAAACAGCAGGTTAGCGGCTGTAAACCAACACCGGTTTCGGCAACAATGACGGGAGAGA	60				
Qy	61	GCCCAACACATTCGATTCGGCTCCGATTAAGCAGCGCCCATTTTCGAGGAGGATT	120				
Db	61	GCCCAACACATTCGATTCGGCTCCGATTAAGCAGCGCCCATTTTCGAGGAGGATT	120				
Qy	121	CGCTCGGTTTGGCGACATTCGGATCCCGGAACAGCTCTGCAATCACTCGCGCGG	180				
Db	121	CGCTCGGTTTGGCGACATTCGGATCCCGGAACAGCTCTGCAATCACTCGCGCGG	180				

Db 3113770 CGCTCGGGTTGGCGACATTCGGATCCCGGAACTAGCTCTGCAATGACCTCGCGCCG 3113711
 QY 181 AGGAAAGCGAGTGGTGGCAGGTTTAAAGCGGTTTAAAGCGTTCGCGGCGAGTGGTG 240
 Db 3113710 AGGAAAGCGAGTGGTGGCAGGTTTAAAGCGGTTTAAAGCGTTCGCGGCGAGTGGTG 3113651
 QY 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTAGTGCATCTTGGCAGAGCATGCACA 300
 Db 3113650 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTAGTGCATCTTGGCAGAGCATGCACA 3113591
 QY 301 ATTCTGAGGGCATAGATTTGCTCGATTTTACAAATGATTTTCAAAAAATA 360
 Db 3113590 ATTCTGAGGGCATAGATTTGCTCGATTTTACAAATGATTTTCAAAAAATA 3113531
 QY 361 ACATTGGTCTGACCATTTTGGGACATTAATCGGCGATTAATAAGGTGTAAACAAAGGA 420
 Db 3113530 ACATTGGTCTGACCATTTTGGGACATTAATCGGCGATTAATAAGGTGTAAACAAAGGA 3113471
 QY 421 ATCGGGCACAAGCTCTTGTGATTTTCTGAGCTGCTTTTGGGTTTGGGTTAGGAA 480
 Db 3113470 ATCGGGCACAAGCTCTTGTGATTTTCTGAGCTGCTTTTGGGTTTGGGTTAGGAA 3113411
 QY 481 ATCAGGAAGTGGGATCGAAA 500
 Db 3113410 ATCAGGAAGTGGGATCGAAA 3113391

RESULT 3
 US-09-738-626-3211/c
 ; Sequence 3211, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 3211
 ; LENGTH: 1776
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-3211

Query Match 52.8%; Score 264; DB 9; Length 1776;
 Best Local Similarity 98.2%; Pred. No. 2.3e-77;
 Matches 267; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 AAAACAGCCAGGTAGCGCTGTAAACCCACCGGTTTCGGCAACATGACGCGGAGAGA 60
 Db 272 AAAACAGCCAGGTAGCGCTGTAAACCCACCGGTTTCGGCAACATGACGCGGAGAGA 213
 QY 61 GCCCACCACATTCGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTTCAGGAGGATT 120
 Db 212 GCCCACCACATTCGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTTCAGGAGGATT 153
 QY 121 CGCTCGGGTTGGCGACATTCGGATCCCGGAAACCGACTCTCTGCAATGACCTCGCGCCG 180

QY 181 AGGAAAGCGAGTGGTGGCAGGTTTAAAGCGGTTTAAAGCGTTCGCGGCGAGTGGTG 240
 Db 181 AGGAAAGCGAGTGGTGGCAGGTTTAAAGCGGTTTAAAGCGTTCGCGGCGAGTGGTG 240
 QY 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTAGTGCATCTTGGCAGAGCATGCACA 300
 Db 241 AGCAAGACGCTAGTCTGGGAGCGGAAACCATATTTAGTGCATCTTGGCAGAGCATGCACA 300
 QY 301 ATTCTGAGGGCATAGATTTGCTCGATTTTACAAATGATTTTCAAAAAATA 360
 Db 301 ATTCTGAGGGCATAGATTTGCTCGATTTTACAAATGATTTTCAAAAAATA 360
 QY 361 ACATTGGTCTGACCATTTTGGGACATTAATCGGCGATTAATAAGGTGTAAACAAAGGA 420
 Db 361 ACATTGGTCTGACCATTTTGGGACATTAATCGGCGATTAATAAGGTGTAAACAAAGGA 420
 QY 421 ATCGGGCACAAGCTCTTGTGATTTTCTGAGCTGCTTTTGGGTTTGGGTTAGGAA 480
 Db 421 ATCGGGCACAAGCTCTTGTGATTTTCTGAGCTGCTTTTGGGTTTGGGTTAGGAA 480
 QY 481 ATCAGGAAGTGGGATCGAAA 500
 Db 481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2
 US-09-738-626-1/c
 ; Sequence 1, Application US/09738626
 ; Publication No. US20020197605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, SATOSHI
 ; APPLICANT: MIZOGUCHI, HIROSHI
 ; APPLICANT: ANDO, SEIKO
 ; APPLICANT: HAYASHI, MIKIRO
 ; APPLICANT: OCHIAI, KEIKO
 ; APPLICANT: YOKOI, HARUHIKO
 ; APPLICANT: TATEISHI, NAOKO
 ; APPLICANT: SENOH, AKIHIRO
 ; APPLICANT: IKEDA, MASATO
 ; APPLICANT: OZAKI, AKIO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-125
 ; CURRENT APPLICATION NUMBER: US/09/738,626
 ; CURRENT FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: JP 99/377484
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: JP 00/159162
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: JP 00/280988
 ; PRIOR FILING DATE: 2000-08-03
 ; NUMBER OF SEQ ID NOS: 7059
 ; SOFTWARE: PatentIn ver. 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3309400
 ; TYPE: DNA
 ; ORGANISM: Corynebacterium glutamicum
 US-09-738-626-1

Query Match 98.1%; Score 490.4; DB 9; Length 3309400;
 Best Local Similarity 98.8%; Pred. No. 1.7e-151;
 Matches 494; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AAAACAGCCAGGTAGCGCTGTAAACCCACCGGTTTCGGCAACATGACGCGGAGAGA 60
 Db 3113890 AAAACAGCCAGGTAGCGCTGTAAACCCACCGGTTTCGGCAACATGACGCGGAGAGA 3113831
 QY 61 GCCCACCACATTCGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTTCAGGAGGATT 120
 Db 3113830 GCCCACCACATTCGGATTTCCGCTCCGATTAAGCCAGCGCCCATATTTTCAGGAGGATT 3113771
 QY 121 CGCTCGGGTTGGCGACATTCGGATCCCGGAAACCGACTCTCTGCAATGACCTCGCGCCG 180

152 GGCCTGCGGTTTGGCGACATTCGGATCCCCGGACTAGCTCTGCAATGACCTGCGCGCG 93

181 AGGAAAGCAGCTGGGTGGCAGGTTTTAGTCGGGTTTTAAGCGTTTGGCCAGGCGAGTGGTG 240

92 AGGAGCGCAGGTGGGTGGCAGGTTTTAGTCGGGTTTTAAGCGTTTGGCCAGGCGAGTGGTG 33

241 AGCAAGACGCTAGTCTGGGAGCGAAACCAT 272

32 AGCAGAGACGCTAGTCTGGGAGCGAAACCAT 1

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RESULT 4
US-10-142-426-10
; Sequence 10, Application US/10142426
; Publication No. US20040048333A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33081C224
; CURRENT APPLICATION NUMBER: US/10/142,426
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-426-10

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Query Match	7.5%;	Score 37.6;	DB 13;	Length 594;
Best Local Similarity	8.7%;	Pred. No. 0.13;		
Matches 23;	Conservative 115;	Mismatches 127;	Indels 0;	Gaps 0;
QY	7	GCACGTTAGCGGCTGTAACCCACACACGCTTTCGGCAACAATGACGGCGAGAGAGCCAC	66	
Db	229	GMADGDFVRLMKDEEAEAIKHALEBEKAMYSGRRSRORREFRKLGRKTSPPS	288	
QY	67	CACATTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTGCAGGAGGATTTCGCCTG	126	
Db	289	YARRDSPYDPKRSFSSSSSRSRSRSPTPGREBEKITFTTTFSGSDEAAAAA	348	
QY	127	CGGTTTGGCGACATTCGGATCCCGGAACACGACTCTGCAATACCTGCGCGCCAGGGAA	186	
Db	349	SGVITGKPPAPPQGPAPGRNASRRSSSSSSSSASPTSSSRSSSRSSSRSGGY	408	
QY	187	GCAGGTGGTGCGAGGTTTATGTCGGGTTTAAAGCTTCCACGCGAGTGTTGACAAA	246	
Db	409	YRSGRHARSRSWSRSRSRRYRSRSRGRHSGGSRDGHYRSRSPARRGGYFRRR	468	
QY	247	GACGTAGTCTGGGAGCGCAACCA	271	
Db	469	SRSRSHSGDFYRRGGRGLFHHSSSR	493	

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US-10-123-155-10
; Sequence 10, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-10

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RESULT 6
US-10-146-731-10
; Sequence 10, Application US/10146731
; Publication No. US2003012962A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

Db 229 GMAAGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRQREFREKRLGRKISPPS 288
QY 67 CACATTGCGATTCCGCTCGGATAAGCAGCCCATATTTCCAGGAGGATTCGCTG 126
Db 289 YARSDPTDYPYKRSSESSESRSRSTPTGREKTIITFSFGSDEAAAAA 348
QY 127 CGGTTGGCGACATTCGGATCCCGGAACAGCAGCTCTGCAATGACCTCGCGCGAGGAA 186
Db 349 SGVTTCKPAPQPGGAPGRNASARRSSSSSSASRTSSRSRSTRRGY 408
QY 187 GCGAGTGGTGGCAGGTTTGTAGCGGTTTAAAGCGTTGCCAGGCGAGTGGTGACAA 246
Db 409 YRSGRHARSRSWSRSRSTRSRSGRRHSGGSRDGHYRSRSPARRGGYGP 468
QY 247 GAGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493

RESULT 9

US-10-142-885-10
; Sequence 10, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-885-10

Query Match 7.5%; Score 37.6; DB 15; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;
QY 7 GCGAGTTAGCGGCTGTAAACCACCGCTTTCGGCAACATGACGCGGAGAGCCAC 66
Db 229 GMAAGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRQREFREKRLGRKISPPS 288
QY 67 CACATTGCGATTCCGCTCGGATAAGCAGCCCATATTTCCAGGAGGATTCGCTG 126
Db 289 YARSDPTDYPYKRSSESSESRSRSTPTGREKTIITFSFGSDEAAAAA 348
QY 127 CGGTTGGCGACATTCGGATCCCGGAACAGCAGCTCTGCAATGACCTCGCGCGAGGAA 186
Db 349 SGVTTCKPAPQPGGAPGRNASARRSSSSSSASRTSSRSRSTRRGY 408
QY 187 GCGAGTGGTGGCAGGTTTGTAGCGGTTTAAAGCGTTGCCAGGCGAGTGGTGACAA 246

Db 409 YRSGRHARSRSWSRSRSTRSRSGRRHSGGSRDGHYRSRSPARRGGYGP 468
QY 247 GAGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493

RESULT 10

US-10-158-790-10
; Sequence 10, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; CURRENT FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-10

Query Match 7.5%; Score 37.6; DB 15; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;
QY 7 GCGAGTTAGCGGCTGTAAACCACCGCTTTCGGCAACATGACGCGGAGAGCCAC 66
Db 229 GMAAGDFVRLMKDKEAEAIKHALEBEKAMYSGRSRRRRQREFREKRLGRKISPPS 288
QY 67 CACATTGCGATTCCGCTCGGATAAGCAGCCCATATTTCCAGGAGGATTCGCTG 126
Db 289 YARSDPTDYPYKRSSESSESRSRSTPTGREKTIITFSFGSDEAAAAA 348
QY 127 CGGTTGGCGACATTCGGATCCCGGAACAGCAGCTCTGCAATGACCTCGCGCGAGGAA 186
Db 349 SGVTTCKPAPQPGGAPGRNASARRSSSSSSASRTSSRSRSTRRGY 408
QY 187 GCGAGTGGTGGCAGGTTTGTAGCGGTTTAAAGCGTTGCCAGGCGAGTGGTGACAA 246
Db 409 YRSGRHARSRSWSRSRSTRSRSGRRHSGGSRDGHYRSRSPARRGGYGP 468
QY 247 GAGCTAGTCTGGGAGCGAAACCA 271
Db 469 SRSRSHGDRYRGRGLRHSSSR 493

RESULT 11

US-10-137-871-10
; Sequence 10, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

Qy 67 CACATTCGATTCCGCTCCGATAAACGCCAGCGCCATATTTTCAGGGAGGATTCGCCTG 126
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 289 YARRDSPTYDKRSPSESSSRKRSRPTPGREEKITFTISFGSDDEAAAAAAAAA 348

RESULT 13
US-10-141-756-10
; Sequence 10, Application US/10141756
; Publication No. US20030207359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Oiang

```

/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P330R1C200
/ CURRENT APPLICATION NUMBER: US/10/141,756
/ CURRENT FILING DATE: 2002-05-08
/ Prior Application removed - See file Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 10
/ LENGTH: 594
/ TYPE: PRT

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Db      289 YARRDSFTYDPKYRSPSESSSRSRSPPTPREKEKITPITSFGGSDERAAAAAAAAA 348

QY     127 CGGTGGTGGCAGATTCGGATCCCGGAACAGACTCTGCATATGACCTGCCGCGCAGGGAA 186
       :|||:           :   :   :   :   :   :   :   :   :   :   :   :
Db      349 SGVTTCKPPAPPQPGGPAPGRNASARRRSSSSSSASRTSSRSRSSRSRSGGY 408

QY     187 GCGAGTGCGTGCGCAGTTTTACTGCGGGTTTAAGCGTTGCCAGCGCAGTGGTAGCAAA 246
       :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db      409 YRSGRHARSRSWSRSRSRYSRYSRGRHRHSGGSRDGHRYSRSPARRGGYGPRR 468

QY     247 GAGCTAGTCTGGGAGCGAAACCA 271
       :||||: | : ||| : | : : : : : : : : : | : ||| :
Db      469 SRSRSHGDRYRGRLRHHSRR 493


RESULT 15
US-10-140-805-10
; Sequence 10, Application US/10140805
; Publication No. US20030207417A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C176
; CURRENT APPLICATION NUMBER: US/10/140,805
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRF
; ORGANISM: Homo Sapien
; US-10-140-805-10

Query Match          7.5%; Score 37.6; DB 16; Length 594;
Best Local Similarity 8.7%; Pred. No. 0.13;
Matches 23; Conservative 115; Mismatches 127; Indels 0; Gaps 0;

QY     7 GCGAGTTAGCGCTGTACCACCGCATTCGGGTTTCGGCAACAATGCGCGCAGAGAGCCCAC 66
       |:|:|: | : : : | : : : : : : : : : : : : : : : :
Db    229 GMADGFVRMLRKDXEAEAIKHALEEBEKAMYSGRSRRQRREFREKLGRKISPPS 288

QY     67 CACATTGCGNATTCGCTCCGATAAACCGCACGCCCATATTTCCAGCGGAGGATTCCGCTG 126
       :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db    289 YARRDSFTYDPKYRSPSESSSRSRSPPTPREKEKITPITSFGGSDERAAAAAAAAA 348

QY     127 CGGTGGTGGCAGATTCGGATCCCGGAACAGACTCTGCATATGACCTGCCGCGCAGGGAA 186
       :|||:           :   :   :   :   :   :   :   :   :   :   :   :
Db      349 SGVTTCKPPAPPQPGGPAPGRNASARRRSSSSSSASRTSSRSRSSRSRSGGY 408

QY     187 GCGAGTGCGTGCGCAGTTTTACTGCGGGTTTAAGCGTTGCCAGCGCAGTGGTAGCAAA 246
       :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db      409 YRSGRHARSRSWSRSRSRYSRYSRGRHRHSGGSRDGHRYSRSPARRGGYGPRR 468

QY     247 GAGCTAGTCTGGGAGCGAAACCA 271
       :||||: | : ||| : | : : : : : : : : : | : ||| :
Db      469 SRSRSHGDRYRGRLRHHSRR 493
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Search completed: August 4, 2004, 14:28:42
Job time : 323 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 13:25:32 ; Search time 2121 Seconds
(without alignments)
10217.594 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
Sequence: 1 aaaaacagcaggttagcgcc.....atcaggaaagtggaatcgaaa 500

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.ov.*

5: gb.pat.*

6: gb.ph.*

7: gb.pl.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.ba.*

15: em.fun.*

16: em.hum.*

17: em.in.*

18: em.mu.*

19: em.ov.*

20: em.or.*

21: em.ov.*

22: em.pat.*

23: em.ph.*

24: em.pl.*

25: em.ro.*

26: em.sts.*

27: em.un.*

28: em.vi.*

29: em.htg.hum.*

30: em.htg.inv.*

31: em.htg.inv.*

32: em.htg.inv.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vit.*

38: em.gv.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	500	100.0	500	6	AX431553	Sequence
C 2	275	55.0	309400	6	AX127153	Sequence
C 3	275	55.0	325651	1	AP005283	Corynebac
C 4	134	26.8	1776	6	AX123295	Sequence
C 5	134	26.8	1776	6	BD165412	Novel pol
6	112	22.4	1084	6	AX763278	Sequence
7	100	20.0	1065	6	AX065003	Sequence
C 8	23	4.6	146505	8	F21M12	Sequence
C 9	21	4.2	816	3	AF302055	Ceratosol
C 10	20	4.0	8729	8	AF076155	Arabidops
C 11	20	4.0	25230	3	U88174	Caenorhabdi
C 12	20	4.0	28577	3	AF000264	Caenorhabdi
C 13	20	4.0	34309	3	CEC05A9	Caenorhabdi
C 14	20	4.0	98535	10	AL928690	Mouse DNA
C 15	20	4.0	103244	3	AC090524	Caenorhab
16	20	4.0	154174	5	AL935239	Zebrafish
17	20	4.0	169258	10	AC132324	Mus muscu
18	20	4.0	171813	2	AC022722	Homo sapi
19	20	4.0	172801	2	AC110908	Mus muscu
20	20	4.0	174632	2	BX897657	Danio rer
21	20	4.0	179071	2	AC146665	Homo sapi
C 22	20	4.0	180035	2	AC142504	Mus muscu
C 23	20	4.0	181833	9	CNS05TEN	Human chr
C 24	20	4.0	187487	2	AC147509	Mus muscu
25	20	4.0	193781	2	AC138282	Mus muscu
26	20	4.0	194596	2	AC140365	Mus muscu
27	20	4.0	195897	2	AC123873	Mus muscu
28	20	4.0	203526	2	AC124606	Mus muscu
29	20	4.0	208587	10	AC124599	Mus muscu
30	20	4.0	211189	2	AC140234	Mus muscu
31	20	4.0	211584	2	AC141645	Mus muscu
32	20	4.0	214574	2	AC124589	Mus muscu
C 33	20	4.0	216667	10	AC125326	Mus muscu
C 34	20	4.0	216911	2	AC126035	Mus muscu
C 35	20	4.0	217825	10	AC132950	Mus muscu
C 36	20	4.0	249688	2	AC126446	Mus muscu
C 37	20	4.0	257013	10	AC114915	Mus muscu
C 38	20	4.0	261333	2	AC138280	Mus muscu
C 39	20	4.0	287664	2	AC109210	Mus muscu
C 40	20	4.0	346516	2	AC138181	Mus muscu
C 41	19	3.8	628	11	HS369F10	STS from
C 42	19	3.8	725	11	BV056433	S212P6531
C 43	19	3.8	852	6	BD186721	Nucleic a
C 44	19	3.8	1024	5	AF217081	Takydromu
C 45	19	3.8	1225	3	AF200389	Ceratosol
46	19	3.8	1829	3	AF200387	Ceratosol
C 47	19	3.8	2027	3	AB051154	Macaca fa
C 48	19	3.8	6971	6	AX344652	Sequence
C 49	19	3.8	7501	1	AE002162	Sequence
50	19	3.8	7502	1	CTPLORF	Chlamydia m
C 51	19	3.8	15373	6	AX345369	Sequence
52	19	3.8	22690	1	AB030032	Actinobac
53	19	3.8	23112	1	AB010415	Actinobac
C 54	19	3.8	27210	9	HS422E10	Human DNA
55	19	3.8	34372	3	U58727	Caenorhabdi
56	19	3.8	37282	3	CEB38A1	Caenorhabdi
57	19	3.8	44237	3	CER05H10	Caenorhabdi
58	19	3.8	50793	2	AC129176	Mus muscu
59	19	3.8	55299	3	AC024830	Caenorhab
C 60	19	3.8	72421	2	AC101509	Mus muscu
C 61	19	3.8	86428	2	AC126016	Medicago
C 62	19	3.8	93407	9	AC011383	Homo sapi
C 63	19	3.8	104186	5	BX088536	Zebrafish
64	19	3.8	107733	9	AC008472	Homo sapi
C 65	19	3.8	110000	3	AC116984_3	Continuation (4 of

C 66	19	3.8	110602	2	AL358592	Homo sapi	139	18	3.6	1923	14	AB064414
C 67	19	3.8	114501	2	AP005093	Oryza sat	140	18	3.6	1961	14	D78433
C 68	19	3.8	118955	9	AC068274	Homo sapi	C 141	18	3.6	2000	6	AX655128
C 69	19	3.8	122051	2	AC146664	Medicago	142	18	3.6	2010	14	FUCHAM
C 70	19	3.8	122051	2	AC146664	Medicago	143	18	3.6	2706	6	AX086825
C 71	19	3.8	133860	2	AL157709	Human DNA	C 144	18	3.6	2706	6	AX086825
C 72	19	3.8	133860	2	AL157709	Human DNA	C 145	18	3.6	2713	6	AX086825
C 73	19	3.8	137525	8	AP005397	Oryza sat	C 146	18	3.6	2713	6	AX086825
C 74	19	3.8	139035	9	AL356102	Human DNA	C 147	18	3.6	2727	9	AX057287
C 75	19	3.8	142123	9	AC004690	Homo sapi	C 148	18	3.6	2727	9	AX057287
C 76	19	3.8	143968	2	AC116117	Mus muscu	C 149	18	3.6	3257	3	AF056111
C 77	19	3.8	149933	9	HSBA37535	Human DNA	C 150	18	3.6	3257	3	AF056111
C 78	19	3.8	150312	9	CNS0198Z	Human DNA	C 151	18	3.6	3293	3	AF069242
C 79	19	3.8	151171	2	AC020775	Homo sapi	C 152	18	3.6	3373	9	HSB06801
C 80	19	3.8	156820	2	AC136266	Rattus no	C 153	18	3.6	3812	10	AF132672
C 81	19	3.8	157545	2	AL163535	Homo sapi	C 154	18	3.6	4025	10	AF127798
C 82	19	3.8	161871	2	AC136912	Mus muscu	C 155	18	3.6	4131	3	AGA535206
C 83	19	3.8	162342	9	AC009041	Homo sapi	C 156	18	3.6	5491	8	ATATKI
C 84	19	3.8	162342	9	AC009041	Homo sapi	C 157	18	3.6	5491	8	ATATKI
C 85	19	3.8	162342	9	AC009041	Homo sapi	C 158	18	3.6	5491	8	ATATKI
C 86	19	3.8	162342	9	AC009041	Homo sapi	C 159	18	3.6	5491	8	ATATKI
C 87	19	3.8	162342	9	AC009041	Homo sapi	C 160	18	3.6	5491	8	ATATKI
C 88	19	3.8	167424	2	AC111075	Mus muscu	C 161	18	3.6	5491	8	ATATKI
C 89	19	3.8	167424	2	AC111075	Mus muscu	C 162	18	3.6	5491	8	ATATKI
C 90	19	3.8	167424	2	AC111075	Mus muscu	C 163	18	3.6	5491	8	ATATKI
C 91	19	3.8	167424	2	AC111075	Mus muscu	C 164	18	3.6	5491	8	ATATKI
C 92	19	3.8	167424	2	AC111075	Mus muscu	C 165	18	3.6	5491	8	ATATKI
C 93	19	3.8	167424	2	AC111075	Mus muscu	C 166	18	3.6	5491	8	ATATKI
C 94	19	3.8	167424	2	AC111075	Mus muscu	C 167	18	3.6	5491	8	ATATKI
C 95	19	3.8	167424	2	AC111075	Mus muscu	C 168	18	3.6	5491	8	ATATKI
C 96	19	3.8	167424	2	AC111075	Mus muscu	C 169	18	3.6	5491	8	ATATKI
C 97	19	3.8	167424	2	AC111075	Mus muscu	C 170	18	3.6	5491	8	ATATKI
C 98	19	3.8	167424	2	AC111075	Mus muscu	C 171	18	3.6	5491	8	ATATKI
C 99	19	3.8	167424	2	AC111075	Mus muscu	C 172	18	3.6	5491	8	ATATKI
C 100	19	3.8	167424	2	AC111075	Mus muscu	C 173	18	3.6	5491	8	ATATKI
C 101	19	3.8	167424	2	AC111075	Mus muscu	C 174	18	3.6	5491	8	ATATKI
C 102	19	3.8	167424	2	AC111075	Mus muscu	C 175	18	3.6	5491	8	ATATKI
C 103	19	3.8	167424	2	AC111075	Mus muscu	C 176	18	3.6	5491	8	ATATKI
C 104	19	3.8	167424	2	AC111075	Mus muscu	C 177	18	3.6	5491	8	ATATKI
C 105	19	3.8	167424	2	AC111075	Mus muscu	C 178	18	3.6	5491	8	ATATKI
C 106	19	3.8	167424	2	AC111075	Mus muscu	C 179	18	3.6	5491	8	ATATKI
C 107	19	3.8	167424	2	AC111075	Mus muscu	C 180	18	3.6	5491	8	ATATKI
C 108	19	3.8	167424	2	AC111075	Mus muscu	C 181	18	3.6	5491	8	ATATKI
C 109	19	3.8	167424	2	AC111075	Mus muscu	C 182	18	3.6	5491	8	ATATKI
C 110	19	3.8	167424	2	AC111075	Mus muscu	C 183	18	3.6	5491	8	ATATKI
C 111	19	3.8	167424	2	AC111075	Mus muscu	C 184	18	3.6	5491	8	ATATKI
C 112	19	3.8	167424	2	AC111075	Mus muscu	C 185	18	3.6	5491	8	ATATKI
C 113	19	3.8	167424	2	AC111075	Mus muscu	C 186	18	3.6	5491	8	ATATKI
C 114	19	3.8	167424	2	AC111075	Mus muscu	C 187	18	3.6	5491	8	ATATKI
C 115	19	3.8	167424	2	AC111075	Mus muscu	C 188	18	3.6	5491	8	ATATKI
C 116	19	3.8	167424	2	AC111075	Mus muscu	C 189	18	3.6	5491	8	ATATKI
C 117	19	3.8	167424	2	AC111075	Mus muscu	C 190	18	3.6	5491	8	ATATKI
C 118	19	3.8	167424	2	AC111075	Mus muscu	C 191	18	3.6	5491	8	ATATKI
C 119	19	3.8	167424	2	AC111075	Mus muscu	C 192	18	3.6	5491	8	ATATKI
C 120	19	3.8	167424	2	AC111075	Mus muscu	C 193	18	3.6	5491	8	ATATKI
C 121	19	3.8	167424	2	AC111075	Mus muscu	C 194	18	3.6	5491	8	ATATKI
C 122	19	3.8	167424	2	AC111075	Mus muscu	C 195	18	3.6	5491	8	ATATKI
C 123	19	3.8	167424	2	AC111075	Mus muscu	C 196	18	3.6	5491	8	ATATKI
C 124	19	3.8	167424	2	AC111075	Mus muscu	C 197	18	3.6	5491	8	ATATKI
C 125	19	3.8	167424	2	AC111075	Mus muscu	C 198	18	3.6	5491	8	ATATKI
C 126	19	3.8	167424	2	AC111075	Mus muscu	C 199	18	3.6	5491	8	ATATKI
C 127	19	3.8	167424	2	AC111075	Mus muscu	C 200	18	3.6	5491	8	ATATKI
C 128	19	3.8	167424	2	AC111075	Mus muscu	C 201	18	3.6	5491	8	ATATKI
C 129	19	3.8	167424	2	AC111075	Mus muscu	C 202	18	3.6	5491	8	ATATKI
C 130	19	3.8	167424	2	AC111075	Mus muscu	C 203	18	3.6	5491	8	ATATKI
C 131	19	3.8	167424	2	AC111075	Mus muscu	C 204	18	3.6	5491	8	ATATKI
C 132	19	3.8	167424	2	AC111075	Mus muscu	C 205	18	3.6	5491	8	ATATKI
C 133	19	3.8	167424	2	AC111075	Mus muscu	C 206	18	3.6	5491	8	ATATKI
C 134	19	3.8	167424	2	AC111075	Mus muscu	C 207	18	3.6	5491	8	ATATKI
C 135	19	3.8	167424	2	AC111075	Mus muscu	C 208	18	3.6	5491	8	ATATKI
C 136	19	3.8	167424	2	AC111075	Mus muscu	C 209	18	3.6	5491	8	ATATKI
C 137	19	3.8	167424	2	AC111075	Mus muscu	C 210	18	3.6	5491	8	ATATKI
C 138	19	3.8	167424	2	AC111075	Mus muscu	C 211	18	3.6	5491	8	ATATKI

AB064414	Influenza
D78433	Influenza C
AX655128	Sequence
M1640	Influenza C
AX086825	Sequence
AL136855	Homo sapi
AX174712	Sequence
AX057287	Homo sapi
BC060798	Homo sapi
AY069242	Grosophila
AX641061	Homo sapi
AF132672	Rattus no
AF127798	Rattus no
AJ352506	Anopheles
X79279	A.thaliana
U51049	Drosophila
AX795936	Sequence
AX822456	Sequence
AX826096	Sequence
M85149	Caenorhabdi
AX346860	Sequence
AC073653	Homo sapi
AC017330	Drosophila
AE014236	Streptoco
Z82059	Caenorhabdi
US3339	Caenorhabdi
AB020747	Arabidops
U21309	Caenorhabdi
U80453	Caenorhabdi
AC002052	Homo sapi
AX602196	Sequence
AC084559	Caenorhab
U39472	Caenorhabdi
Z81039	Caenorhabdi
Z81071	Caenorhabdi
Z75530	Caenorhabdi
AC131484	Lytechinu
AC015272	Lytechinu
Continuation (4 of	
AC014068	Drosophila
AC009913	Drosophila
AC134685	Homo sapi
AC131486	Lytechinu
AC135651	Rattus no
AL645603	Mouse DNA
AL356416	Human DNA
AC013253	Homo sapi
AC080081	Homo sapi
Continuation (4 of	
AL354879	Human DNA
AB010075	Arabidops
AB010075	Arabidops
AL1390726	Human DNA
AL17399	Homo sapi
AL139231	Human DNA
AL096764	Human DNA
AL096692	Arabidops
AP002020	Homo sapi
AP003222	Oryza sat
AL513363	Human DNA
AC112695	Homo sapi
Continuation (3 of	
Continuation (5 of	
AL021684	Arabidops
AC126283	Homo sapi
AC092575	Homo sapi
AC144472	Felis cat
AC119409	Medicago
AC145165	Medicago
AC007616	Homo sapi
AP003297	Oryza sat
AC090795	Homo sapi

C 212	18	3.6	139292	2	AC103397	Mus muscu	AC103397	18	C 285	3.6	181777	2	AC068866	Homo sapi
C 213	18	3.6	139407	9	AL627310	Human DNA	AL627310	18	C 286	3.6	181980	2	AC011827	Homo sapi
C 214	18	3.6	141568	9	AC063956	Homo sapi	AC063956	18	C 287	3.6	182163	2	AC000690	Danio rer
C 215	18	3.6	141868	9	AC107980	Homo sapi	AC107980	18	C 288	3.6	182960	3	AC010017	Drosophila
C 216	18	3.6	143747	9	HS370M22	Human DNA	HS370M22	18	C 289	3.6	183394	9	AC009102	Homo sapi
C 217	18	3.6	144619	2	AC012465	Homo sapi	AC012465	18	C 290	3.6	183422	2	AC006905	Caenorhab
C 218	18	3.6	146258	2	AC023479	Homo sapi	AC023479	18	C 291	3.6	183460	9	AL356753	Human DNA
C 219	18	3.6	147438	2	AC146990	Lytechinu	AC146990	18	C 292	3.6	185918	9	AC009839	Drosophila
C 220	18	3.6	148068	1	AB001488	Bacillus	AB001488	18	C 293	3.6	186755	9	AC094022	Homo sapi
C 221	18	3.6	148342	9	AC010140	Homo sapi	AC010140	18	C 294	3.6	187268	9	AC094022	Homo sapi
C 222	18	3.6	150054	9	AL161901	Human DNA	AL161901	18	C 295	3.6	188459	3	AC008312	Drosophila
C 223	18	3.6	151559	9	AL390294	Human DNA	AL390294	18	C 296	3.6	189308	9	AC093416	Homo sapi
C 224	18	3.6	152634	2	AC114626	Mus muscu	AC114626	18	C 297	3.6	192203	9	AC034102	Homo sapi
C 225	18	3.6	152878	3	CEV18D10A	Caenorhab	AC103493	18	C 298	3.6	192404	2	AC027769	Homo sapi
C 226	18	3.6	153819	10	AC121955	Mus muscu	AC121955	18	C 299	3.6	193099	2	AC027769	Homo sapi
C 227	18	3.6	153903	9	AC008380	Homo sapi	AC008380	18	C 300	3.6	193099	9	AC092140	Homo sapi
C 228	18	3.6	153906	9	AC008503	Homo sapi	AC008503	18	C 301	3.6	194378	2	AL645770	Homo sapi
C 229	18	3.6	154386	2	AC016314	Homo sapi	AC016314	18	C 302	3.6	194431	2	AC107853	Mus muscu
C 230	18	3.6	154386	2	AL356474	Homo sapi	AL356474	18	C 303	3.6	194916	9	AL138921	Human DNA
C 231	18	3.6	155001	2	AC024048	Homo sapi	AC024048	18	C 304	3.6	195912	1	BSUB0003	299106 Bacillus su
C 232	18	3.6	158126	2	AC024048	Homo sapi	AC024048	18	C 305	3.6	195912	3	AC011253	AC011253 Drosophila
C 233	18	3.6	158792	8	AP005696	Oryza sat	AP005696	18	C 306	3.6	197597	2	AC011253	AC011253 Drosophila
C 234	18	3.6	158857	2	AC023522	Homo sapi	AC023522	18	C 307	3.6	199196	2	AC011253	AC011253 Drosophila
C 235	18	3.6	159115	9	AC006406	Homo sapi	AC006406	18	C 308	3.6	199711	10	AC117217	AC117217 Mus muscu
C 236	18	3.6	159144	2	AC018783	Homo sapi	AC018783	18	C 309	3.6	199956	10	AC007550	AC007550 Mus muscu
C 237	18	3.6	159351	2	AC116564	Homo sapi	AC116564	18	C 310	3.6	200001	8	ATCHRIV71	ATCHRIV71 Arabidops
C 238	18	3.6	159435	9	AL136231	Human DNA	AL136231	18	C 311	3.6	201124	2	AC074287	AC074287 Homo sapi
C 239	18	3.6	160012	2	AC145042	Macropus	AC145042	18	C 312	3.6	201305	5	AC117437	AC117437 Homo sapi
C 240	18	3.6	160333	2	AC145042	Macropus	AC145042	18	C 313	3.6	201305	5	AC117437	AC117437 Homo sapi
C 241	18	3.6	160836	2	EX470097	Danio rer	EX470097	18	C 314	3.6	201448	5	EX284620	EX284620 Zebrafish
C 242	18	3.6	160836	2	EX470097	Danio rer	EX470097	18	C 315	3.6	205029	2	AC118189	AC118189 Rattus no
C 243	18	3.6	161527	2	AC024676	Homo sapi	AC024676	18	C 316	3.6	205816	9	AC013751	AC013751 Homo sapi
C 244	18	3.6	161827	2	AC139668	Papio ham	AC139668	18	C 317	3.6	209633	2	AC107733	AC107733 Mus muscu
C 245	18	3.6	161938	9	CNS0180Y	Human chr	AL109769	18	C 318	3.6	210674	2	AC131521	AC131521 Rattus no
C 246	18	3.6	163400	9	AC010364	Homo sapi	AC010364	18	C 319	3.6	213294	2	AC110326	AC110326 Rattus no
C 247	18	3.6	164480	9	AC112493	Homo sapi	AC112493	18	C 320	3.6	216244	10	AL732321	AL732321 Mouse DNA
C 248	18	3.6	164631	2	AC022356	Homo sapi	AC022356	18	C 321	3.6	216272	2	AC092712	AC092712 Mus muscu
C 249	18	3.6	165604	4	AC091722	Sus scrof	AC091722	18	C 322	3.6	216393	2	AC115662	AC115662 Rattus no
C 250	18	3.6	165746	5	EX510652	Zebrafish	EX510652	18	C 323	3.6	216474	2	AC139414	AC139414 Rattus no
C 251	18	3.6	166049	2	AC037470	Homo sapi	AC037470	18	C 324	3.6	217323	2	AC115724	AC115724 Mus muscu
C 252	18	3.6	166317	9	AL157895	Human DNA	AL157895	18	C 325	3.6	217567	10	AC125177	AC125177 Mus muscu
C 253	18	3.6	166704	9	AC078797	Homo sapi	AC078797	18	C 326	3.6	217794	2	AC111124	AC111124 Mus muscu
C 254	18	3.6	167346	9	AC096640	Homo sapi	AC096640	18	C 327	3.6	218584	2	AC097559	AC097559 Rattus no
C 255	18	3.6	168023	2	AC016084	Homo sapi	AC016084	18	C 328	3.6	219408	2	AC140216	AC140216 Mus muscu
C 256	18	3.6	168023	2	AC137786	Homo sapi	AC137786	18	C 329	3.6	220469	2	AC074307	AC074307 Mus muscu
C 257	18	3.6	168161	2	AC012687	Homo sapi	AC012687	18	C 330	3.6	222163	10	AL731558	AL731558 Mouse DNA
C 258	18	3.6	168515	5	AL954143	Zebrafish	AL954143	18	C 331	3.6	222722	2	AC095588	AC095588 Rattus no
C 259	18	3.6	168843	2	AC091711	Rattus no	AC091711	18	C 332	3.6	223349	5	EX649612	EX649612 Zebrafish
C 260	18	3.6	169032	2	AL356431	Homo sapi	AL356431	18	C 333	3.6	225038	2	AC111507	AC111507 Rattus no
C 261	18	3.6	170331	9	AC025419	Homo sapi	AC025419	18	C 334	3.6	226298	2	AC144902	AC144902 Mus muscu
C 262	18	3.6	170681	10	AC112271	Mus muscu	AC112271	18	C 335	3.6	226494	2	AC096527	AC096527 Rattus no
C 263	18	3.6	170923	2	AC016181	Homo sapi	AC016181	18	C 336	3.6	228448	2	AC096527	AC096527 Rattus no
C 264	18	3.6	170928	9	AC034148	Homo sapi	AC034148	18	C 337	3.6	230421	2	AC106984	AC106984 Rattus no
C 265	18	3.6	171798	2	AC084397	Trypanoso	AC084397	18	C 338	3.6	230828	2	AC105632	AC105632 Rattus no
C 266	18	3.6	172272	9	AC027804	Homo sapi	AC027804	18	C 339	3.6	231507	2	AC137434	AC137434 Rattus no
C 267	18	3.6	172568	9	AC007016	Homo sapi	AC007016	18	C 340	3.6	232779	2	EX601648	EX601648 Danio rer
C 268	18	3.6	173533	2	AL136144	Homo sapi	AL136144	18	C 341	3.6	232874	2	AC114223	AC114223 Rattus no
C 269	18	3.6	173591	2	AC140351	Mus muscu	AC140351	18	C 342	3.6	233050	1	SAG766848	AL766848 Streptoco
C 270	18	3.6	174387	9	AC092350	Homo sapi	AC092350	18	C 343	3.6	233115	2	EX640548	EX640548 Danio rer
C 271	18	3.6	175940	9	AL109918	Human DNA	AL109918	18	C 344	3.6	234426	2	AC128724	AC128724 Rattus no
C 272	18	3.6	176233	2	AC102885	Mus muscu	AC102885	18	C 345	3.6	235075	2	AC137044	AC137044 Rattus no
C 273	18	3.6	177097	10	AC132303	Mus muscu	AC132303	18	C 346	3.6	239053	2	AC129055	AC129055 Rattus no
C 274	18	3.6	177608	3	AC099553	Drosophila	AC099553	18	C 347	3.6	242400	2	AC096829	AC096829 Rattus no
C 275	18	3.6	177722	2	AL158053	Human DNA	AL158053	18	C 348	3.6	245387	2	AL358052	AL358052 Homo sapi
C 276	18	3.6	177839	2	EX530075	Danio rer	EX530075	18	C 349	3.6	246670	2	AC111872	AC111872 Rattus no
C 277	18	3.6	178001	10	AL772227	Mouse DNA	AL772227	18	C 350	3.6	246962	2	AC073811	AC073811 Mus muscu
C 278	18	3.6	178362	9	AL355615	Human DNA	AL355615	18	C 351	3.6	247467	2	AC118508	AC118508 Rattus no
C 279	18	3.6	178374	2	EX677667	Danio rer	EX677667	18	C 352	3.6	249131	2	AC121717	AC121717 Rattus no
C 280	18	3.6	179283	3	AC009383	Drosophila	AC009383	18	C 353	3.6	251567	2	AC117020	AC117020 Rattus no
C 281	18	3.6	179601	2	AC101702	Mus muscu	AC101702	18	C 354	3.6	260279	2	AC142066	AC142066 Rattus no
C 282	18	3.6	179879	2	AC026883	Homo sapi	AC026883	18	C 355	3.6	260341	3	CEY116A8C	CEY116A8C Caenorhab
C 283	18	3.6	180364	2	EX548247	Danio rer	EX548247	18	C 356	3.6	262930	2	AC113753	AC113753 Rattus no
C 284	18	3.6	181446	2	AC067813	Homo sapi	AC067813	18	C 357	3.6	267795	2	AC096390	AC096390 Rattus no

358	18	3..6	270169	2	AC103230	AC103230 Rattus no	431	17	3..4	10233	1	AE011023	AE011023 Methanos
359	18	3..6	272329	2	AC094789	AC094789 Rattus no	C 432	17	3..4	10356	9	AC093380	AC093380 Homo sapi
360	18	3..6	272329	2	AC094789	AC094789 Rattus no	C 433	17	3..4	10661	1	AE006119	AE006119 Pasteurel
361	18	3..6	273105	2	AC112439	AC112439 Rattus no	C 434	17	3..4	10757	1	AE008389	AE008389 Streptoco
362	18	3..6	276719	2	AC111548	AC111548 Rattus no	C 435	17	3..4	10882	1	AE007322	AE007322 Streptoco
363	18	3..6	298700	1	AP005951	AP005951 Bradyrhiz	C 436	17	3..4	11032	1	AE0013267	AE0013267 Methanos
364	18	3..6	299903	3	AE003514	AE003514 Drosophill	C 437	17	3..4	11296	1	AE001030	AE001030 Archaeogl
365	18	3..6	300217	1	AE016922	AE016922 Chromobac	C 438	17	3..4	11301	1	AE0007492	AE0007492 Streptoco
366	18	3..6	300511	1	AE016775	AE016775 Clostridi	C 439	17	3..4	11443	6	AR218817	AR218817 Sequence
367	18	3..6	301439	1	AE015943	AE015943 Pseudomon	C 440	17	3..4	11443	6	BD003729	BD003729 Polynucle
368	18	3..6	301838	1	AE017209	AE017209 Geobacter	C 441	17	3..4	11937	6	AE012277	AE012277 Xanthomon
369	18	3..6	308435	2	AC099254	AC099254 Rattus no	C 442	17	3..4	12503	8	CL2MRPB	CL2MRPB Zea mays ch
370	18	3..6	314306	3	AE003594	AE003594 Drosophill	C 443	17	3..4	12855	1	AE007455	AE007455 Streptoco
371	18	3..6	315752	2	AC120285	AC120285 Rattus no	C 444	17	3..4	14277	3	CEY44A6B	CEY44A6B Caenorhab
372	18	3..6	315844	3	AE003671	AE003671 Drosophill	C 445	17	3..4	14619	3	CEP58D12	CEP58D12 Caenorhab
373	18	3..6	324688	2	AC111620	AC111620 Rattus no	C 446	17	3..4	17913	10	WU278574	WU278574 Mus muscu
374	18	3..6	325265	2	AC111802	AC111802 Rattus no	C 447	17	3..4	18420	2	AC017154	AC017154 Drosophill
375	18	3..6	349742	1	BX572090	BX572090 Prochloro	C 448	17	3..4	19292	3	CEY76A2A	CEY76A2A Caenorhab
376	18	3..6	349980	6	AX344573	AX344573 Sequence	C 449	17	3..4	20539	9	HS349E10	HS349E10 Human DNA
377	17	3..4	558	11	G94778	G94778 S208P6807RE	450	17	3..4	21245	8	AB027572	AB027572 Triticum
378	17	3..4	645	6	BD064358	BD064358 Novel cod	451	17	3..4	22724	10	BX470094	BX470094 Mouse DNA
379	17	3..4	648	11	BV056832	BV056832 S212P6827	452	17	3..4	24711	3	AF039036	AF039036 Caenorhab
380	17	3..4	696	6	AX194063	AX194063 Sequence	C 453	17	3..4	25245	3	AF040644	AF040644 Caenorhab
381	17	3..4	720	6	AX194289	AX194289 Sequence	C 454	17	3..4	25750	3	AF016413	AF016413 Caenorhab
382	17	3..4	744	6	AX570108	AX570108 Sequence	C 455	17	3..4	25777	3	AC024828	AC024828 Caenorhab
383	17	3..4	764	11	BV024119	BV024119 S212P6031	C 456	17	3..4	28466	3	U88171	U88171 Caenorhab
384	17	3..4	965	6	AX753003	AX753003 Sequence	C 457	17	3..4	28473	6	AR218851	AR218851 Sequence
385	17	3..4	969	1	AF485768	AF485768 Aeromonas	C 458	17	3..4	29145	10	AF127669	AF127669 Mus muscu
386	17	3..4	1013	9	HSNKKE	X00187 Human prepr	C 459	17	3..4	32575	9	AL596115	AL596115 Human DNA
387	17	3..4	1203	9	F202550S15	AF202564 Homo sapi	C 460	17	3..4	32970	3	U58760	U58760 Caenorhab
388	17	3..4	1219	10	MDL132555	BD132555 Mus platy	C 461	17	3..4	32970	3	U58760	U58760 Caenorhab
389	17	3..4	1243	6	MDL190961	BD190961 DNA methy	C 462	17	3..4	32970	3	U58760	U58760 Caenorhab
390	17	3..4	1329	1	STRPURISYN	LI5190 Streptococc	C 463	17	3..4	32970	3	U58760	U58760 Caenorhab
391	17	3..4	1602	6	AX764604	AX764604 Sequence	C 464	17	3..4	32970	3	U58760	U58760 Caenorhab
392	17	3..4	1703	10	BC029630	BC029630 Mus muscu	C 465	17	3..4	32970	3	U58760	U58760 Caenorhab
393	17	3..4	1768	9	D50001S01	D50001 Homo sapien	C 466	17	3..4	32970	3	U58760	U58760 Caenorhab
394	17	3..4	1813	6	AR379862	AR379862 Sequence	C 467	17	3..4	32970	3	U58760	U58760 Caenorhab
395	17	3..4	2106	8	AF013693	AF013693 Codonanth	C 468	17	3..4	32970	3	U58760	U58760 Caenorhab
396	17	3..4	2119	3	AF159419	AF159419 Drosophill	C 469	17	3..4	32970	3	U58760	U58760 Caenorhab
397	17	3..4	2414	6	AX878253	AX878253 Sequence	C 470	17	3..4	32970	3	U58760	U58760 Caenorhab
398	17	3..4	2414	6	BD157110	BD157110 Primer fo	C 471	17	3..4	32970	3	U58760	U58760 Caenorhab
399	17	3..4	2414	9	AK002141	AK002141 Homo sapi	C 472	17	3..4	32970	3	U58760	U58760 Caenorhab
400	17	3..4	2528	1	AE002141	M84709 Aeromonas h	C 473	17	3..4	32970	3	U58760	U58760 Caenorhab
401	17	3..4	2546	6	A94935	A94935 Sequence 20	C 474	17	3..4	32970	3	U58760	U58760 Caenorhab
402	17	3..4	2763	5	CHKPECM	BC040316 Homo sapi	C 475	17	3..4	32970	3	U58760	U58760 Caenorhab
403	17	3..4	2872	9	BC040316	BC040316 Homo sapi	C 476	17	3..4	32970	3	U58760	U58760 Caenorhab
404	17	3..4	2877	6	BD227594	BD227594 C. albica	C 477	17	3..4	32970	3	U58760	U58760 Caenorhab
405	17	3..4	2877	6	BD227594	BD227594 C. albica	C 478	17	3..4	32970	3	U58760	U58760 Caenorhab
406	17	3..4	3109	6	AX833797	AX833797 Sequence	C 479	17	3..4	32970	3	U58760	U58760 Caenorhab
407	17	3..4	3109	9	AK095811	AK095811 Homo sapi	C 480	17	3..4	32970	3	U58760	U58760 Caenorhab
408	17	3..4	3272	8	AK110021	AK110021 Oryza sat	C 481	17	3..4	32970	3	U58760	U58760 Caenorhab
409	17	3..4	3666	3	AX155564	AX155564 Ochlerota	C 482	17	3..4	32970	3	U58760	U58760 Caenorhab
410	17	3..4	3672	8	ACH132014	AJ132014 Acremoniu	C 483	17	3..4	32970	3	U58760	U58760 Caenorhab
411	17	3..4	3726	6	AX571586	AX571586 Sequence	C 484	17	3..4	32970	3	U58760	U58760 Caenorhab
412	17	3..4	3925	2	AK124692	AK124692 Homo sapi	C 485	17	3..4	32970	3	U58760	U58760 Caenorhab
413	17	3..4	3978	2	AC017659	AC017659 Drosophill	C 486	17	3..4	32970	3	U58760	U58760 Caenorhab
414	17	3..4	4565	8	D78336	D78336 Oryza sativ	C 487	17	3..4	32970	3	U58760	U58760 Caenorhab
415	17	3..4	4852	1	PSU05130	U25130 Pseudomonas	C 488	17	3..4	32970	3	U58760	U58760 Caenorhab
416	17	3..4	4871	9	HSA278993	HSA278993 Homo sapi	C 489	17	3..4	32970	3	U58760	U58760 Caenorhab
417	17	3..4	4940	9	AF180682	AF180682 Homo sapi	C 490	17	3..4	32970	3	U58760	U58760 Caenorhab
418	17	3..4	5165	3	DROCOPIA	D10880 Drosophilla	C 491	17	3..4	32970	3	U58760	U58760 Caenorhab
419	17	3..4	5434	6	AX330730	AX330730 Sequence	C 492	17	3..4	32970	3	U58760	U58760 Caenorhab
420	17	3..4	5434	6	AX330939	AX330939 Sequence	C 493	17	3..4	32970	3	U58760	U58760 Caenorhab
421	17	3..4	5434	6	AX332235	AX332235 Sequence	C 494	17	3..4	32970	3	U58760	U58760 Caenorhab
422	17	3..4	5434	5	HSDNMTASE	X63692 H. sapiens m	C 495	17	3..4	32970	3	U58760	U58760 Caenorhab
423	17	3..4	5455	5	U00455	U00455 Acipenser t	C 496	17	3..4	32970	3	U58760	U58760 Caenorhab
424	17	3..4	5771	6	AX346853	AX346853 Sequence	C 497	17	3..4	32970	3	U58760	U58760 Caenorhab
425	17	3..4	6069	9	HSU42391	U42391 Human myosi	C 498	17	3..4	32970	3	U58760	U58760 Caenorhab
426	17	3..4	8471	1	TRMFSNA	M36180 Streptococc	C 499	17	3..4	32970	3	U58760	U58760 Caenorhab
427	17	3..4	8028	8	TOMFSPG	M87659 Tomato frui	C 500	17	3..4	32970	3	U58760	U58760 Caenorhab
428	17	3..4	9905	6	AX344964	AX344964 Sequence	C 501	17	3..4	32970	3	U58760	U58760 Caenorhab
429	17	3..4	9975	1	AE001048	AE001048 Archaeogl	C 502	17	3..4	32970	3	U58760	U58760 Caenorhab
430	17	3..4	10029	1	AE008548	AE008548 Streptoco	C 503	17	3..4	32970	3	U58760	U58760 Caenorhab

504	17	3.4	59228	2	AC069452	AC069452 Homo sapi	577	17	3.4	110000	2	EX323988_0	EX323988 Danio rer
505	17	3.4	59533	3	AC084450	AC084450 Caenorhab	c 578	17	3.4	110000	2	CEY105E8_3	Continuation (4 of
506	17	3.4	61017	2	AC099990	AC099990 Mus muscu	c 579	17	3.4	110000	2	CEY111B2_2	Continuation (3 of
507	17	3.4	61448	2	AC100679	AC100679 Mus muscu	c 580	17	3.4	110000	3	AC125735_0	AC125735 Leishmani
508	17	3.4	63949	9	AC005903	AC005903 Homo sapi	c 581	17	3.4	110000	6	AR406002_1	Continuation (2 of
509	17	3.4	64258	8	BX842595	BX842595 Neurospor	c 582	17	3.4	110000	8	AC145127_17	Continuation (18 o
510	17	3.4	64667	10	BX0000436	BX0000436 Mouse DNA	c 583	17	3.4	110000	8	AC145127_18	Continuation (19 o
511	17	3.4	69308	2	AC011539	AC011539 Mus muscu	c 584	17	3.4	110000	10	AE014176_2	Continuation (3 of
512	17	3.4	69577	2	AC014098	AC014098 Drosophil	c 585	17	3.4	111477	9	AL451162	AL451162 Human DNA
513	17	3.4	69814	2	AC129565	AC129565 Mus muscu	c 586	17	3.4	113098	2	AC009458	AC009458 Drosophil
514	17	3.4	70694	3	AC006708	AC006708 Caenorhab	c 587	17	3.4	113250	9	AC004900	AC004900 Homo sapi
515	17	3.4	73145	2	AC009767	AC009767 Homo sapi	c 588	17	3.4	116821	9	AL606537	AL606537 Human DNA
516	17	3.4	73169	2	AC100699	AC100699 Mus muscu	c 589	17	3.4	117026	9	HS329A5	Z97832 Human DNA s
517	17	3.4	73233	2	AC116222	AC116222 Rattus no	c 590	17	3.4	117751	9	AC020913	AC020913 Homo sapi
518	17	3.4	73233	2	AC116222	AC116222 Rattus no	c 591	17	3.4	117751	9	AC012349	AC012349 Homo sapi
519	17	3.4	74990	2	AC024421	AC024421 Homo sapi	c 592	17	3.4	118405	9	AC012349	Z83836 Human DNA s
520	17	3.4	75125	8	AB025604	AB025604 Arabidops	c 593	17	3.4	119008	9	HS111J24	HS111J24
521	17	3.4	77422	3	AC025723	AC025723 Caenorhab	c 594	17	3.4	120027	2	AC020981	AC020981 Homo sapi
522	17	3.4	77439	9	HS127F18	AL031575 Human DNA	c 595	17	3.4	121143	8	AC144484	AC144484 Medicago
523	17	3.4	77673	2	AC120790	AC120790 Mus muscu	c 596	17	3.4	121609	2	AC137653	AC137653 Bos tauru
524	17	3.4	78153	3	CEY53C10A	AL033536 Caenorhab	c 597	17	3.4	121902	9	AC008386	AC008386 Homo sapi
525	17	3.4	78449	9	AC141965	AC141965 Rattus no	c 598	17	3.4	122916	9	AL162716	AL162716 Human DNA
526	17	3.4	81207	9	HS125I13	AL033528 Human DNA	c 599	17	3.4	124836	9	AC003085	AC003085 Homo sapi
527	17	3.4	81250	9	AC124298	AC124298 Homo sapi	c 600	17	3.4	125590	3	CEY49E10	Z98866 Caenorhabdi
528	17	3.4	81239	2	AC140044	AC140044 Mus muscu	c 601	17	3.4	125798	9	AL3900248	AL3900248 Human DNA
529	17	3.4	84615	9	AL354747	AL354747 Human DNA	c 602	17	3.4	125936	8	AC122148	AC122148 Oryza sat
530	17	3.4	85644	3	AC084463	AC084463 Caenorhab	c 603	17	3.4	126708	2	AC118340	AC118340 Genomic s
531	17	3.4	86052	2	AC015946	AC015946 Mus muscu	c 604	17	3.4	126708	2	AC009843	AC009843 Drosophil
532	17	3.4	86141	9	BX323845	BX323845 Human DNA	c 605	17	3.4	127091	8	AC009843	AL050340 Human DNA
533	17	3.4	87635	10	AL929052	AL929052 Mouse DNA	c 606	17	3.4	128235	9	HS7995C14	AL669846 Mouse DNA
534	17	3.4	88382	2	AC018394	AC018394 Homo sapi	c 607	17	3.4	128747	10	AL669846	AL355852 Human DNA
535	17	3.4	88955	9	AY442342	AY442342 Homo sapi	c 608	17	3.4	128765	9	AL355852	AC121233 Medicago
536	17	3.4	89350	8	ATT12H17	AL021635 Arabidops	c 609	17	3.4	129318	8	AC121233	AC148633 Mus muscu
537	17	3.4	89370	3	AC084153	AC084153 Caenorhab	c 610	17	3.4	129503	2	AC044863	AL669940 Mouse DNA
538	17	3.4	89728	9	AL583805	AL583805 Human DNA	c 611	17	3.4	129897	10	AL669940	AC145491 Genomic s
539	17	3.4	90526	9	AC092393	AC092393 Homo sapi	c 612	17	3.4	130656	8	AC145491	AC145414 Felis cat
540	17	3.4	91820	3	AL513547	AL513547 Human DNA	c 613	17	3.4	130765	2	AC145414	AC145414 Felis cat
541	17	3.4	92613	2	AC084161	AC084161 Caenorhab	c 614	17	3.4	131616	10	AL840632	AL840632 Mouse DNA
542	17	3.4	93159	9	HS106C24	AC011839 Homo sapi	c 615	17	3.4	131704	2	AP004313	AP004313 Oryza sat
543	17	3.4	94734	9	HS232P20	Z83313 Human DNA s	c 616	17	3.4	131704	2	AP004313	AJ277546 Homo sapi
544	17	3.4	94770	9	HSJ657D12	AL019943 Human DNA	c 617	17	3.4	131998	9	AC138779	AC138779 Homo sapi
545	17	3.4	95449	9	AP001620	AP001620 Homo sapi	c 618	17	3.4	132010	2	AC024351	AC024351 Homo sapi
546	17	3.4	96955	6	AX695617	AX695617 Sequence	c 619	17	3.4	132191	9	AC073332	AC073332 Homo sapi
547	17	3.4	96642	9	AC002291	AC002291 Arabidops	c 620	17	3.4	132396	2	BX571845	AC024351 Homo sapi
548	17	3.4	97711	8	ATT16K5	AL132965 Arabidops	c 621	17	3.4	132508	8	AC006778	AC024351 Homo sapi
549	17	3.4	97995	9	AC067718	AC067718 Homo sapi	c 622	17	3.4	132749	2	AC006778	AC134967 Medicago
550	17	3.4	99897	9	AC093584	AC093584 Homo sapi	c 623	17	3.4	133028	8	AL136325	AL136325 Human DNA
551	17	3.4	100369	9	AL139258	AL139258 Human DNA	c 624	17	3.4	133052	8	AC092553	AC092553 Oryza sat
552	17	3.4	101216	2	AC110722	AC110722 Danio rer	c 625	17	3.4	133121	8	AC092553	Oryza sat
553	17	3.4	101565	8	AC145753	AC145753 Genomic s	c 626	17	3.4	133421	8	AP005469	AP005469 Oryza sat
554	17	3.4	102008	2	AC016552	AC016552 Homo sapi	c 627	17	3.4	134273	8	AP005469	X15901 Oryza sativ
555	17	3.4	103040	9	AC104966	AC104966 Homo sapi	c 628	17	3.4	134525	8	AB042240	AB042240 Triticum
556	17	3.4	103069	9	AL606469	AL606469 Human DNA	c 629	17	3.4	134545	8	AB042240	AC013788 Homo sapi
557	17	3.4	105211	9	AC110076	AC110076 Homo sapi	c 630	17	3.4	134867	2	AC092750	AC092750 Oryza sat
558	17	3.4	105392	9	AC073215	AC073215 Homo sapi	c 631	17	3.4	134985	2	AC146941	AC092750 Oryza sat
559	17	3.4	105600	8	AP005173	AP005173 Oryza sat	c 632	17	3.4	134985	2	AC146941	AC146941 Medicago
560	17	3.4	107044	9	AC011375	AC011375 Homo sapi	c 633	17	3.4	135050	2	AC118536	AC118536 Canis fam
561	17	3.4	107238	9	AC106786	AC106786 Homo sapi	c 634	17	3.4	135252	5	BX119965	BX119965 Zebrafish
562	17	3.4	107714	2	AL356306	AL356306 Homo sapi	c 635	17	3.4	135252	5	BX119965	AC084761 Gallus ga
563	17	3.4	108158	8	ATF3A4	AL132978 Arabidops	c 636	17	3.4	135286	10	AL928905	AL928905 Mouse DNA
564	17	3.4	109148	2	AC138439	AC138439 Takifugu	c 637	17	3.4	135286	10	AL928905	AL354809 Human DNA
565	17	3.4	110000	2	AC095863	Continuation (3 of	c 638	17	3.4	135619	9	AL354809	AL50426 Human DNA
566	17	3.4	110000	2	AC106698	Continuation (3 of	c 639	17	3.4	136022	9	AL450426	AL50426 Human DNA
567	17	3.4	110000	2	AC111622	Continuation (3 of	c 640	17	3.4	136022	9	AL450426	AC067916 Homo sapi
568	17	3.4	110000	2	AC118304	Continuation (3 of	c 641	17	3.4	136228	2	AC132483	AC067916 Homo sapi
569	17	3.4	110000	2	AC118330	Continuation (3 of	c 642	17	3.4	136787	2	AC132483	AC132483 Oryza sat
570	17	3.4	110000	2	AC120922	Continuation (3 of	c 643	17	3.4	137259	2	AC010392	AC010392 Homo sapi
571	17	3.4	110000	2	AC120932	Continuation (3 of	c 644	17	3.4	137515	2	DMBR12B22	AL122029 Drosophil
572	17	3.4	110000	2	AC139489	Continuation (3 of	c 645	17	3.4	137724	8	AC122147	AC122147 Oryza sat
573	17	3.4	110000	2	AC139489	Continuation (3 of	c 646	17	3.4	137724	8	AC122147	AC004884 Homo sapi
574	17	3.4	110000	2	AC140148	Continuation (2 of	c 647	17	3.4	138244	9	AC004884	AL41002 Homo sapi
575	17	3.4	110000	2	AC142490	Continuation (2 of	c 648	17	3.4	138981	9	AL41002	AL158048 Human DNA
576	17	3.4	110000	2	AC146445	Continuation (2 of	c 649	17	3.4	139111	9	AL158048	AC011750 Homo sapi
	17	3.4	110000	2	AC146445	Continuation (2 of	c 650	17	3.4	139111	9	AL158048	AC011750 Homo sapi
	17	3.4	110000	2	AC146445	Continuation (2 of	c 651	17	3.4	139166	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 652	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 653	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 654	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 655	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 656	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 657	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 658	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 659	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 660	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 661	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 662	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 663	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 664	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 665	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 666	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 667	17	3.4	139712	9	AC011750	AC145828 Pan trogl
	17	3.4	110000	2	AC146445	Continuation (2 of	c 668	17	3.4				

c 650	17	3.4 140403	2	AC109444	AC109444 Homo sapi	723	17	3.4 154888	2	BX897659	BX897659 Danio rer
651	17	3.4 140763	2	AC144549	AC144549 Sorghum b	c 724	17	3.4 154931	2	BX649585	BX649585 Danio rer
c 652	17	3.4 140854	9	AC108038	Homo sapi	c 725	17	3.4 154995	9	AC011979	AC011979 Homo sapi
c 653	17	3.4 141432	2	AC015699	AC015699 Homo sapi	c 726	17	3.4 155334	2	AC011156	AC011156 Homo sapi
c 654	17	3.4 141899	9	AC087457	AC087457 Homo sapi	c 727	17	3.4 155411	10	AC133602	AC133602 Mus muscu
c 655	17	3.4 141925	2	AC098702	AC098702 Felis cat	c 728	17	3.4 155510	2	AL353723	AL353723 Homo sapi
656	17	3.4 142420	8	AP005813	AP005813 Human DNA	729	17	3.4 155642	3	AC091228	AC091228 Drosophil
c 657	17	3.4 142510	8	AP005813	AP005813 Oryza sat	730	17	3.4 156249	2	BX276184	BX276184 Danio rer
c 658	17	3.4 142638	9	AL355316	AL355316 Human DNA	c 731	17	3.4 156249	2	BX276184	BX276184 Danio rer
c 659	17	3.4 142641	9	AC132068	AC132068 Homo sapi	732	17	3.4 156441	9	AC091869	AC091869 Homo sapi
c 660	17	3.4 143065	2	AC105375	AC105375 Felis cat	733	17	3.4 156677	2	AC092550	AC092550 Homo sapi
c 661	17	3.4 143283	9	AC016763	AC016763 Homo sapi	734	17	3.4 156955	2	AP001908	AP001908 Homo sapi
c 662	17	3.4 143487	2	AC141129	AC141129 Rattus no	735	17	3.4 157080	2	AL358856	AL358856 Homo sapi
c 663	17	3.4 143798	9	AL157409	AL157409 Human DNA	736	17	3.4 157390	2	BX324227	BX324227 Danio rer
c 664	17	3.4 143878	9	AC003074	AC003074 Homo sapi	737	17	3.4 157722	10	AL953890	AL953890 Mouse DNA
c 665	17	3.4 143893	2	AC010766	AC010766 Homo sapi	738	17	3.4 157788	2	AV178786	AV178786 Canis fam
c 666	17	3.4 144410	2	AC012084	AC012084 Mus muscu	c 739	17	3.4 157792	9	AC069209	AC069209 Homo sapi
c 667	17	3.4 144734	2	AP001839	AP001839 Homo sapi	c 740	17	3.4 157833	9	AC132186	AC132186 Homo sapi
c 668	17	3.4 145980	8	OSJN00291	BX569685 Oryza sat	c 741	17	3.4 157891	10	AC133161	AC133161 Mus muscu
c 669	17	3.4 146083	8	AP003315	AP003315 Oryza sat	c 742	17	3.4 158027	10	AC125093	AC125093 Mus muscu
c 670	17	3.4 146099	2	AC011192	AC011192 Homo sapi	743	17	3.4 158034	2	AC019275	AC019275 Homo sapi
c 671	17	3.4 146112	9	HS592A1	AL035411 Human DNA	c 744	17	3.4 158091	9	AC140171	AC140171 Homo sapi
c 672	17	3.4 146144	8	AP003331	AP003331 Oryza sat	c 745	17	3.4 158264	2	AC015497	AC015497 Homo sapi
c 673	17	3.4 146275	2	AC080119	AC080119 Homo sapi	746	17	3.4 158312	2	AC083922	AC083922 Homo sapi
c 674	17	3.4 146464	5	BX530024	BX530024 Zebraphish	747	17	3.4 158401	2	AC068521	AC068521 Homo sapi
c 675	17	3.4 146699	9	BS000226	BS000226 Pan trogl	c 748	17	3.4 158544	2	AC023658	AC023658 Homo sapi
c 676	17	3.4 146708	2	BX321881	BX321881 Mus muscu	c 749	17	3.4 158736	2	AC021109	AC021109 Homo sapi
c 677	17	3.4 146961	2	AL355525	AL355525 Homo sapi	750	17	3.4 158966	2	AC113296	AC113296 Mus muscu
c 678	17	3.4 147207	2	AC078890	AC078890 Oryza sat	c 751	17	3.4 158983	3	AC005374	AC005374 Drosophil
c 679	17	3.4 147310	2	AL513495	AL513495 Homo sapi	752	17	3.4 159150	2	AC104279	AC104279 Oryza sat
c 680	17	3.4 147500	8	AP004849	AP004849 Oryza sat	753	17	3.4 159300	9	HS279F22	AL662879 Homo sapi
c 681	17	3.4 147663	2	AC118259	AC118259 Mus muscu	c 754	17	3.4 159312	2	AC096878	AC096878 Pan trogl
c 682	17	3.4 147728	2	AC034113	AC034113 Homo sapi	755	17	3.4 159438	2	AC016621	AC016621 Homo sapi
c 683	17	3.4 148115	2	AC125498	AC125498 Danio rer	c 756	17	3.4 159445	9	AC092994	AC092994 Homo sapi
c 684	17	3.4 148248	2	RN235J17	AL603722 Rattus no	c 757	17	3.4 159656	5	AL329243	AL329243 Zebraphish
c 685	17	3.4 148347	8	AP005408	AP005408 Oryza sat	c 758	17	3.4 159676	2	AC145299	AC145299 Mus muscu
c 686	17	3.4 148347	8	AP005408	AP005408 Oryza sat	c 759	17	3.4 159784	2	AC061996	AC061996 Homo sapi
c 687	17	3.4 148704	8	AC124213	AC124213 Genomic s	760	17	3.4 160096	2	AC022657	AC022657 Homo sapi
c 688	17	3.4 149338	2	AC129836	AC129836 Felis cat	c 761	17	3.4 160145	9	AL161612	AL161612 Human DNA
c 689	17	3.4 149618	9	AP000556	AP000556 Homo sapi	c 762	17	3.4 160283	9	AC011773	AC011773 Homo sapi
c 690	17	3.4 149622	2	AC074082	AC074082 Homo sapi	763	17	3.4 160370	9	AC023464	AC023464 Homo sapi
c 691	17	3.4 149910	9	AC023391	AC023391 Homo sapi	c 764	17	3.4 160370	9	AC074029	AC074029 Homo sapi
c 692	17	3.4 150036	9	AP000557	AP000557 Homo sapi	765	17	3.4 161103	9	AL392163	AL392163 Human DNA
c 693	17	3.4 150728	9	AC084277	AC084277 Homo sapi	c 766	17	3.4 161180	2	AC146771	AC146771 Canis fam
c 694	17	3.4 150728	9	AC021297	AC021297 Homo sapi	767	17	3.4 161306	2	AC091056	AC091056 Homo sapi
c 695	17	3.4 150817	8	AP003323	AP003323 Oryza sat	768	17	3.4 161348	10	AL645532	AL645532 Mouse DNA
c 696	17	3.4 151142	9	AC069275	AC069275 Homo sapi	769	17	3.4 161366	9	AC090939	AC090939 Homo sapi
c 697	17	3.4 151143	9	AC108714	AC108714 Homo sapi	c 770	17	3.4 161366	9	AC093657	AC093657 Homo sapi
c 698	17	3.4 151173	8	AC135257	AC135257 Genomic s	771	17	3.4 161942	2	BX322538	BX322538 Danio rer
c 699	17	3.4 151242	2	AC144589	AC144589 Homo sapi	c 772	17	3.4 162023	9	AC084033	AC084033 Homo sapi
c 700	17	3.4 151267	8	AC134932	AC134932 Oryza sat	773	17	3.4 162100	9	AC018868	AC018868 Homo sapi
c 701	17	3.4 151733	2	AC079643	AC079643 Mus muscu	774	17	3.4 162209	9	CNS01R1H	AL163195 Human chr
c 702	17	3.4 151753	2	AC119614	AC119614 Rattus no	c 775	17	3.4 162457	2	BX000523	BX000523 Danio rer
c 703	17	3.4 151973	2	OSJN00178	AL662978 Oryza sat	c 776	17	3.4 162564	10	AC127575	AC127575 Mus muscu
c 704	17	3.4 152058	4	AC091756	AC091756 Sus scrof	c 777	17	3.4 162689	9	AC093657	AC093657 Homo sapi
c 705	17	3.4 152123	2	AC046190	AC046190 Homo sapi	c 778	17	3.4 162714	2	AC027569	AC027569 Homo sapi
c 706	17	3.4 152295	2	AC139615	AC139615 Rattus no	c 779	17	3.4 162727	9	HS46711	Z98884 Human DNA s
c 707	17	3.4 152519	2	AC108898	AC108898 Felis cat	780	17	3.4 162778	2	AC009559	AC009559 Homo sapi
c 708	17	3.4 152547	2	AC118934	AC118934 Mus muscu	781	17	3.4 162837	2	AC142143	AC142143 Medicago
c 709	17	3.4 152910	8	AP005537	AP005537 Oryza sat	c 782	17	3.4 162955	9	AC012527	AC012527 Homo sapi
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 c 976 17 3.4 192267 8 AC092748
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 978 17 3.4 192591 2 AC107739
 c 979 17 3.4 192621 2 AC115010
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ALIGNMENTS

RESULT 1
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 DEFINITION Sequence 7 from Patent WO240679.
 ACCESSION AX431553
 VERSION AX431553.1 GI:21656357
 KEYWORDS Corynebacterium glutamicum
 ORGANISM Corynebacterium glutamicum

linear PAT 28-JUN-2002

REFERENCE 1
 AUTHORS Crafton, C.M. and Rayapati, P.J.
 TITLE Nucleotide sequences for transcriptional regulation in Corynebacterium glutamicum
 JOURNAL Patent: WO 0240679-A 7 23-MAY-2002;
 CRAFTON COREY M (US); RAYAPATI P JOHN (US)
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RESULT 2
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 DEFINITION Sequence 7069 from Patent EP1108790.
 ACCESSION AX127153
 VERSION AX127153.1 GI:14041141
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Corynebacterium glutamicum

REFERENCE 1
 AUTHORS Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
 TITLE Novel polynucleotides
 JOURNAL Patent: EP 1108790-A 7069 20-JUN-2001;
 KYOWA HAKKO KOGYO CO., LTD. (JP)

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.

Crafton, C.M. and Rayapati, P.J.
 Nucleotide sequences for transcriptional regulation in
 Corynebacterium glutamicum

Patent: WO 0240679-A 7 23-MAY-2002;
 CRAFTON COREY M (US); RAYAPATI P JOHN (US)

Location/Qualifiers
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Query Match 100.0%; Score 500; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 4e-298;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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 DEFINITION Sequence 7069 from Patent EP1108790.
 ACCESSION AX127153
 VERSION AX127153.1 GI:14041141
 KEYWORDS
 SOURCE
 ORGANISM
 Corynebacterium glutamicum
 Corynebacterium glutamicum

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Corynebacteriaceae; Corynebacterium.

Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
 Novel polynucleotides
 Patent: EP 1108790-A 7069 20-JUN-2001;
 KYOWA HAKKO KOGYO CO., LTD. (JP)


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KEYWORDS
SOURCE      Corynebacterium glutamicum
ORGANISM    Corynebacterium glutamicum
            Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE
AUTHORS     Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE       Novel polynucleotides
JOURNAL     Patent: EP 1108790-A 3211 20-JUN-2003;
            KYOWA HAKKO KOGYO CO., LTD. (JP)
FEATURES
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Query Match      26.8%; Score 134; DB 6; Length 1776;
Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 GTAACCCACCCACGGTTTCGGCAACAATGACGCGGAGAGAGCCACACATTCGGATTTC 81
Db 251 GTAACCCACCCACGGTTTCGGCAACAATGACGCGGAGAGAGCCACACATTCGGATTTC 192
QY 82 GTCCTGATTAAGCCAGCGCCCATATTTGCAGGAGGATTTCGCTCGGTTTGGCGACATT 141
Db 191 GTCCTGATTAAGCCAGCGCCCATATTTGCAGGAGGATTTCGCTCGGTTTGGCGACATT 132
QY 142 CGGATCCCCGGGAAC 155
Db 131 CGGATCCCCGGGAAC 118
RESULT 5
LOCUS      BD165412/5
DEFINITION Novel polynucleotide.
ACCESSION BD165412
VERSION    BD165412.1 GI:27871224
KEYWORDS   unidentifed
SOURCE     unclassified.
ORGANISM   1 (bases 1 to 1776)
            Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A.
TITLE       Novel polynucleotide
JOURNAL     Patent: JP 2002191370-A 3211 09-JUL-2002;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS Corynebacterium glutamicum
            PN JP 2002191370-A/3211
            PD 09-JUL-2002
            PF 15-DEC-2000 JP 2000405096
            PI SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
            PI KEIKO OCHIAI,
            PI HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
            PI OZAKI
            PC C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00,PC
            C12N1/15,
            PC C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/
            PC 04,C12P13/08,
            PC C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53,PC
            G01N33/566,
            PC G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15),
            PC (C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15),
            PC C12N15/00,
            PC C12N5/00,C12N15/00
            CC Novel polynucleotide
            FH Key
            FT source
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FEATURES
source      Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.2e-71;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 GTAACCCACCCACGGTTTCGGCAACAATGACGCGGAGAGAGCCACACATTCGGATTTC 81
Db 251 GTAACCCACCCACGGTTTCGGCAACAATGACGCGGAGAGAGCCACACATTCGGATTTC 192
QY 82 GTCCTGATTAAGCCAGCGCCCATATTTGCAGGAGGATTTCGCTCGGTTTGGCGACATT 141
Db 191 GTCCTGATTAAGCCAGCGCCCATATTTGCAGGAGGATTTCGCTCGGTTTGGCGACATT 132
QY 142 CGGATCCCCGGGAAC 155
Db 131 CGGATCCCCGGGAAC 118
RESULT 6
LOCUS      AX763278
DEFINITION Sequence 95 from Patent WO03040291.
ACCESSION AX763278
VERSION    AX763278.1 GI:32257846
KEYWORDS   Corynebacterium glutamicum
SOURCE     Corynebacterium glutamicum
            Bacteria; Actinobacteridae; Actinobacteriaceae; Corynebacterium.
REFERENCE
AUTHORS     Zelder,O., Pompejus,M., Schroeder,H., Kroeger,B., Kloppege,C. and
            Haberhauser,G.
TITLE       Genes encoding for carbon metabolism and energy-producing proteins
            Patent: WO 03040291-A 95 15-MAY-2003;
            BASF AKTIENGESSELLSCHAFT (DE)
FEATURES
source      Location/Qualifiers
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            101..1057
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            /db_xref="GI:32257847"
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            RYMLGEYEVAPSVHAYIIGHGTEPLVLSATLIGVSLSRMLDKDPELEGRLEKI
            FEDTDAAYHIIDAKSGSYGICMGLARITRAILQNQDVAVPVSALLHGEYGEDYI
            GTPAVNRRGIRRVVELEITDHEMERFKHSANTLREIQKQF"
            CDS
            101..1057
            /note="unnamed protein product; RXA02694"
ORIGIN
Query Match      22.4%; Score 112; DB 6; Length 1084;
Best Local Similarity 100.0%; Pred. No. 3.6e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 TAATCGGCATATTAAGGTGTAAACAAGGATCCGGGCACAAAGCTCTTGCTGATTTC 448
Db 1 TAATCGGCATATTAAGGTGTAAACAAGGATCCGGGCACAAAGCTCTTGCTGATTTC 60
QY 449 TGAGCTGCTTTGTGGTGTTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 500
Db 61 TGAGCTGCTTTGTGGTGTTCGGTTAGGGAATCAGGAAGTGGGATCGAAA 112

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RESULT 7
AX065003
LOCUS AX065003 1065 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 129 from Patent WO0100844.
ACCESSION AX065003
VERSION AX065003.1 GI:12542715
KEYWORDS
SOURCE
ORGANISM Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
REFERENCE
AUTHORS Pompejus, M., Kroeger, B., Schroeder, H., Zelder, O. and Haberer, G.
TITLE corynebacterium glutamicum genes encoding proteins involved in
carbon metabolism and energy production
JOURNAL Patent: WO 0100844-A 129 04-JAN-2001;
BASIS AKTINGESSELLSCHAFT (DE)
FEATURES
Location/Qualifiers
source 1..1065
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/db_xref="taxon:1718"
101..1045
/feature="unnamed protein product; RXA02694"
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/transl_table="MKETGNGKIVLIGAGDVAVAYALINGMADHLAIIIDIEKLI
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GELYEAPSSVHAYIIIEHGDTELVSSATVAGVLSRLMDKPELGRLEKIFEDT
RDAAYHIIIDKANGTSYIGIMGLRITRAILQNDQVAVPVSVALLHGEYGEEDIIYGTGA
VNRGRIRRVVELEITDHMERFKHSANTLREIQKQFF"
ORIGIN
Query Match 20.0%; Score 100; DB 6; Length 1065;
Best Local Similarity 100.0%; Pred. No. 1e-49;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 401 ATTAAGGTGTAAACAAGGATCCGGCACAAAGCTCTTGCTGATTCTTGAGCTGCTTTG 460
Db 1 ATTAAGGTGTAAACAAGGATCCGGCACAAAGCTCTTGCTGATTCTTGAGCTGCTTTG 60
QY 461 TGGGTTTCGCGTTAGGGAATCAGGAAGTGGGATCGAAA 500
Db 61 TGGGTTTCGCGTTAGGGAATCAGGAAGTGGGATCGAAA 100
RESULT 8
F21M12/c
LOCUS F21M12 146505 bp DNA linear PLN 09-JUN-1997
DEFINITION Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1,
complete sequence.
ACCESSION AC000132
VERSION AC000132.1 GI:2160155
KEYWORDS H7G.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 146505)
Vysotskaya, V.S., Osborne, B.I., Toriumi, M., Yu, G., Oji, O.,
Shen, Y.K., Araujo, R., Au, M., Buehler, E., Conway, A.B., Conway, A.R.,
Dewar, K., Feng, J., Kim, C., Kurtz, D., Li, Y., Shinn, P., Sun, H.,
Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A.
The sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1
Unpublished (1997)
REFERENCE
AUTHORS Theologis, A.
TITLE Direct Submission
JOURNAL
REFERENCE 2 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (28-FEB-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
3 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (18-MAR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
4 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (21-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
5 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (22-APR-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
6 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (02-MAY-1997) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
7 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (29-MAY-1997)
JOURNAL 8 (bases 1 to 146505)
AUTHORS Theologis, A.
TITLE Direct Submission
Submitted (09-JUN-1997)
JOURNAL
COMMENT On Jun 4, 1997 this sequence version replaced gi:2065477.
The sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1.
FEATURES
Location/Qualifiers
source 1..146505
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/chromosome="1"
complement(87..3341)
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complement(87..3341)
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/note="Strong similarity to S. pombe leucyl-trna
synthetase (gb|Z73100)."
/codon_start=1
/evidence="not experimental"
/protein_id="AAB60719.1"
/db_xref="GI:2160156"
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VTSVPDADQYMALQDIKKPALQDKYQEWLPEIPIINIPEFGKAAEKVCL
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IYSEPEKPMVSRSGDECVALTQWVITYGESWRKTAECLSKNLYSDETHGFPH
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CLADAGDVDDANFAPETANAALRLTKLTWMEVLDVDESSLRTGTPPTPYADKVPF
DMNIALRLTERAYDKCLFREALNGFVLDQAARDEVLSCGTGMHDLKLMVDVOT
RLVPLCPHFADVVRKLNKGCGLTAGPSPNEDPLVLSKANKYLODSIVLKRLL
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7845..7946,8057..8546,8659..9038)
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GYRSLGSLGKPLATGYKFWLYNSIEIGLENATTCVEFDFTNAWRVYSPAARYL
VCGPAPVCVGLHWFTCEETKILSFDLTFQVSKAPFANVDGFDIVMCLDNIR
LCVSEMKLPNOVIMFNSGNKTHKWCISINLDITSRWFQGTQVCAVLPALDLGGKKK
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complement(20993..22816)
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VEMVTMCGFLVDALMTYDGLGFIIPAOCFRLSRKRRFDVTRGCGNLLDRMMKL
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KGGY"
complement(24846..27004)

Query Match      4.6%; Score 23; DB 8; Length 146505;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 TTGCTGATTTCTGAGTCGCTTT 459
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Db 86781 TTGCTGATTTCTGAGTCGCTTT 86759

RESULT 9
AF302055 816 bp DNA linear INV 25-JAN-2001
LOCUS Ceratosolen constrictus cytochrome oxidase I (COI) gene, partial
DEFINITION cds; mitochondrial gene for mitochondrial product.
ACCESSION AF302055
VERSION AF302055.1 GI:11245194
KEYWORDS .
SOURCE mitochondrial Ceratosolen constrictus
ORGANISM Ceratosolen constrictus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
Agaonidae; Agaoninae; Ceratosolen.
REFERENCE 1 (bases 1 to 816)
AUTHORS West, S.A., Murray, M.G., Machado, C.A., Griffin, A.S. and Herre, E.A.
TITLE Testing Hamilton's rule with competition between relatives
JOURNAL Nature 409 (6819), 510-513 (2001)
MEDLINE 21074930
PUBMED 11206546
REFERENCE 2 (bases 1 to 816)
AUTHORS Machado, C.A.
TITLE Direct Submission
JOURNAL Submitted (31-AUG-2000) Naos Laboratories, Smithsonian Tropical
RESEARCH Research Institute, Balboa Apartado 2072, Panama
FEATURES
source
1. .816
/organism="Ceratosolen constrictus"
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/specific_host="Ficus fistulosa"
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mRNA
CDS

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FIFLFTGVGVGNLANALDVILHDTYVVAHFHYLSMGAVFAIMGSFVFWFPLIS
GIGLQKLMQFWSLFTGVNFTFPQHFGLSGMPRYSYDPDYMCKNKLISMGAL
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ORIGIN

Query Match 4.2%; Score 21; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 TGATTTTTCACAAATAA 361
Db 722 TGATTTTTCACAAATAA 742

RESULT 10

AF076155/c

LOCUS

DEFINITION

Arabis thaliana CRT/CRE binding factor 1 (CBF1), CRT/DRE

binding factor 3 (CBF3), and CRT/DRE binding factor 2 (CBF2) genes,

complete cds.

AF076155

AF076155.1 GI:4091981

Arabis thaliana (thale cress)

Arabis thaliana

Arabis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 8729)

Gilmour, S.J., Zarka, D.G., Stockinger, E.J., Salazar, M.P.,

Houghton, J.M., and Thomashow, M.F.

Low temperature regulation of the Arabidopsis CBF family of AP2

transcriptional activators as an early step in cold-induced COR

gene expression

Plant J. 16 (4), 433-442 (1998)

9881163

2 (bases 1 to 8729)

Gilmour, S.J., Zarka, D.G., Stockinger, E.J., Salazar, M.P. and

Thomashow, M.F.

Direct Submission

Submitted (29-JUN-1998) Crop and Soil Sciences, Michigan State

University, East Lansing, MI 48824, USA

Location/Qualifiers

1..8729

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/cultivar="Landberg erecta"

/db_xref="taxon:3702"

/chromosome="4"

/map="close to PG11 and m600"

<1443..>2084

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<1443..>2084

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/product="CRT/CRE binding factor 1"

1443..2084

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/note="AP2 transcriptional activator"

/codon_start=1

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/protein_id="AAC99369.1"
/db_xref="GI:4091982"

/translation="MNSFSAESEMFGSDYEPQGGDYCPITLASCCKPKPKRKKR
HPIYRQNRSGKWSVEVPKTRIKWLTGFTQTAEMAAAHDAVAALRGRSACLN
FADSAWRLRIPESCAKDIQAAAALAFQDETCTTTDHDGDMETVVEAIYTP
QSEGAFYMDTEMTFEMPTLLDNMAEGLLPSPVQWNHNYDGGDGVLSWSY"

gene

mRNA

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

CDS

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CDS

CDS

CDS

CDS

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CDS

CDS

ORIGIN

Query Match 4.0%; Score 20; DB 8; Length 8729;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 345 TTTTTCACAAATAACAC 364
Db 3392 TTTTTCACAAATAACAC 3373

RESULT 11

U88174

LOCUS

DEFINITION

Caenorhabditis elegans cosmid M01A10, complete sequence.

U88174

U88174.1 GI:1825651

HTG.

SOURCE

ORGANISM

Caenorhabditis elegans

Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

Rhabditoides; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 25230)

Wilson, R.

Genome sequence of the nematode C. elegans: a platform for

investigating biology. The C. elegans Sequencing Consortium

Science 282 (5396), 2012-2018 (1998)

99069613

2 (bases 1 to 25230)

Scheet, P.

THE SEQUENCE OF C. ELEGANS COSMID M01A10

Unpublished (2001)

3 (bases 1 to 25230)

AUTHORS TITLE JOURNAL		FEATURES source
REFERENCE AUTHORS TITLE JOURNAL	Waterston, R. Direct Submission Submitted (03-FEB-1997) Genome Sequencing Center, Washington University 4 (bases 1 to 25230) Waterston, R. Direct Submission Submitted (25-JUL-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA 5 (bases 1 to 25230) Waterston, R. Direct Submission Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA 6 (bases 1 to 25230) Waterston, R. Direct Submission Submitted (15-JUN-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA Submitted by: Genome Sequencing Center Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 1RQ, England email: submissions@wustl.edu and jessesanger.ac.uk	Location/Qualifiers 1..25230 /organism="Caenorhabditis elegans" /mol_type="genomic DNA" /strain="Bristol N2" /db_xref="taxon:6239" /chromosome="I" /clone="M01A10" 3279..18158 /gene="M01A10.2" Join(3279..3290,3332..3571,4951..5049,5101..5177,5234..5699,5745..5981,7678..7745,7793..7949,8069..8263,8796..8906,8954..9050,9455..9597,9736..10225,11882..12034,14525..14638,16185..16330,16624..16931,17166..17229,17381..17494,17683..17743,17790..17935,18021..18158) /gene="M01A10.2" /standard_name="M01A10.2c" /note="contains similarity to Pfam domain PF00400 (WD domain, G-beta repeats); coded for by the following C. elegans cDNAs: yk1060a12.5, yk1214e06.5" /codon_start=1 /product="Hypothetical protein M01A10.2c" /protein_id="AAP68903.1" /db_xref="GI:31746531" /db_xref="WormBase:M01A10.2c" /translation="MRILVVRHGLPEPRCFAYDPVQRLLAIGTGRGHIRIIGDAGVD YLLKHSEGPVLMQFLVNEGLITSCGTDISHLWNYRQKTAIEVHTVQLSKESVSCI HLPVAGKLVFICTDKGNVFLCLNSFLSPYVNNKADLSCRHPGPVROLAVSPA ENTLLIVYDGIWQNLGTREVDYPLDPIKSNVWDFDGRQILITGNVDGSIISYN HKKSTAIORTPHSGPCRPCIOQVWKHMSSETSIIMFSGMPTDGLDMPALATILK GKGSATVLEMDWPIIOFILPNQINWNSIPQCPSHSAVLKHKDFWLDLQNGHGVIES PHANNIHESPVTCMAYSDCLDILGALTGTQKRNKEFSARSWPTGGLGRECATG HOELVVTGHKDGSLKFWQETGEHLQILYKLKSSHPERLEEMETSKDVHAKVYIELC LESROLLVAGISGQVTLPRFTKQEGCTIAVNIPLLLGNLSMTPNDKDFKVPVNGP KKEIRQRKIVRETSNIDTSDGDERIVPEKVGAPYKRPGRFVPELACFPVPMHSH AKVQITTLINSSYGIATGSSGLAVDTTCQALYISWTTNELYSGDTPAIOISM QJSDAASPLEIDEDEFENDUTLIYNTDGNILKRSNLSPSSNGFLHPGEMPTPKSA ANSNKGGMGLPRNTAEALATIRERYQGNRESATDRDPVHERGTPTPTNEG NKVOKAGRSYKVGSPFIRFAAKTSKKEKYKIEVDNQNSGIERSFPHSHISEG DSORSPSSGROLNTSSPTSSQSLERSMSTQESITSLSFTHYSKNDKMSVCL WYGTSGASLALNLLIPEDRTSTIVAPSGTVRLKGOVISOSEWMDNFTCIISPASE SYKEAKESQATSPORSLNVRNTKASLAPQVSSSIDSDSNDSEISQILIVAEENVKVA LPTFQSLYQKFEDEPLVKATPHINGYPCMLCSAAGQILMSLSRLRLQITSTLFF HSEVIDDPLCQKTADESDHGLVYMAQTEMEKYTCMCEIABQGESLGLFVCEPME QPKNSFLKGVSSIFGCTPRNDPIDAILSENMGVNSGVNPMESVARTIPGPSVQ MRAQAGVYSAGQAAMALQNLNTERKLNATVDATENLKNAMSLSSRTIKLVEKYE KKKWYNF"
REFERENCE AUTHORS TITLE JOURNAL	Waterston, R. Direct Submission Submitted (15-JUN-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA Submitted by: Genome Sequencing Center Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 1RQ, England email: submissions@wustl.edu and jessesanger.ac.uk	CDS Join(3279..3290,3332..3571,4951..5049,5101..5177,5234..5699,5745..5981,7678..7745,7793..7949,8069..8263,8796..8906,8954..9050,9455..9597,11597..11720,11882..12034,14525..14638,16185..16330,16624..16931,17166..17229,17381..17494,17683..17743,17790..17935,18021..18158) /gene="M01A10.2" /standard_name="M01A10.2a" /notes="contains similarity to Pfam domain PF00400 (WD domain, G-beta repeats); coded for by the following C. elegans cDNAs: yk49c3.3, yk49c3.5, yk50g8.3, yk52f2.3, yk52f2.5, CEMS28R, yk223a7.5, yk239c1.3, yk239c1.5, yk406e4.3, yk406e4.5" /codon_start=1 /product="Hypothetical protein M01A10.2a" /protein_id="AAP68902.1" /db_xref="GI:31746530" /db_xref="WormBase:M01A10.2a" /translation="MRILVVRHGLPEPRCFAYDPVQRLLAIGTGRGHIRIIGDAGVD YLLKHSEGPVLMQFLVNEGLITSCGTDISHLWNYRQKTAIEVHTVQLSKESVSCI HLPVAGKLVFICTDKGNVFLCLNSFLSPYVNNKADLSCRHPGPVROLAVSPA ENTLLIVYDGIWQNLGTREVDYPLDPIKSNVWDFDGRQILITGNVDGSIISYN HKKSTAIORTPHSGPCRPCIOQVWKHMSSETSIIMFSGMPTDGLDMPALATILK GKGSATVLEMDWPIIOFILPNQINWNSIPQCPSHSAVLKHKDFWLDLQNGHGVIES PHANNIHESPVTCMAYSDCLDILGALTGTQKRNKEFSARSWPTGGLGRECATG HOELVVTGHKDGSLKFWQETGEHLQILYKLKSSHPERLEEMETSKDVHAKVYIELC
REFERENCE AUTHORS TITLE JOURNAL	Waterston, R. Direct Submission Submitted (15-JUN-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA Submitted by: Genome Sequencing Center Department of Genetics, Washington University St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 1RQ, England email: submissions@wustl.edu and jessesanger.ac.uk	CDS Join(3279..3290,3332..3571,4951..5049,5101..5177,5234..5699,5745..5981,7678..7745,7793..7949,8069..8263,8796..8906,8954..9050,9455..9597,11597..11720,11882..12034,14525..14638,16185..16330,16624..16931,17166..17229,17381..17494,17683..17743,17790..17935,18021..18158) /gene="M01A10.2" /standard_name="M01A10.2a" /notes="contains similarity to Pfam domain PF00400 (WD domain, G-beta repeats); coded for by the following C. elegans cDNAs: yk49c3.3, yk49c3.5, yk50g8.3, yk52f2.3, yk52f2.5, CEMS28R, yk223a7.5, yk239c1.3, yk239c1.5, yk406e4.3, yk406e4.5" /codon_start=1 /product="Hypothetical protein M01A10.2a" /protein_id="AAP68902.1" /db_xref="GI:31746530" /db_xref="WormBase:M01A10.2a" /translation="MRILVVRHGLPEPRCFAYDPVQRLLAIGTGRGHIRIIGDAGVD YLLKHSEGPVLMQFLVNEGLITSCGTDISHLWNYRQKTAIEVHTVQLSKESVSCI HLPVAGKLVFICTDKGNVFLCLNSFLSPYVNNKADLSCRHPGPVROLAVSPA ENTLLIVYDGIWQNLGTREVDYPLDPIKSNVWDFDGRQILITGNVDGSIISYN HKKSTAIORTPHSGPCRPCIOQVWKHMSSETSIIMFSGMPTDGLDMPALATILK GKGSATVLEMDWPIIOFILPNQINWNSIPQCPSHSAVLKHKDFWLDLQNGHGVIES PHANNIHESPVTCMAYSDCLDILGALTGTQKRNKEFSARSWPTGGLGRECATG HOELVVTGHKDGSLKFWQETGEHLQILYKLKSSHPERLEEMETSKDVHAKVYIELC

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

For a graphical representation of this cosmid sequence and its analysis see:
<http://www.wormbase.org/db/seq/sequence?name=M01A10;class=Sequence>

NEIGHBORING COSMID INFORMATION

The 5' cosmid is F59A3, 200 bp overlap; the 3' cosmid is M01E11, 200 bp overlap. Actual start of this cosmid is at base position 27001 of F59A3; actual end is at 4204 of M01E11.

NOTES:

Coding sequences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFome cloning project (<http://wormdb.dfc.harvard.edu/>), similarity to other proteins from BlastX analyses (<http://blast.wustl.edu/>), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans Genbank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Iowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

NOTES:

Coding sequences below are the result of integration and manual review of the following data : computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST project of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFome cloning project (http://worldb.dfc.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"

/strain="Bristol N2"

/db_xref="taxon:6239"

/chromosome="II"

/clone="F43E2"

/complement (28. .2242)

/gene="hsp-4"

/complement (join(28. .132,182. .885,932. .1166,1216. .1782,1832. .2016,2065. .2242))

/gene="hsp-4"

/standard_name="F43E2.8"

/notes="contains similarity to Pfam domain PF00012 (Heat shock hsp70 proteins); coded for by the following C. elegans cDNAs: yk17h11.5, yk285f12.5, yk181e12.5, yk68d12.5, cm06f6, yk34e10.3, yk34e10.5, yk127e8.5, yk160a6.5, yk168a9.5, yk330d2.5, yk333b1.5, yk336e8.5, yk345c11.5, yk374b4.5, yk375c10.5, yk400h2.5, yk421c2.5, yk452h2.5, yk464b2.5, yk464b12.5, yk458e7.5, yk339f10.5, yk414f6.5, yk320a1.5, yk464b2.3, yk415b6.3, yk345c11.3, yk436b11.3, yk374b4.3, yk464b12.3, yk285f12.3, yk458e7.3, yk375c10.3, yk421c2.3, yk339f10.3, yk336e8.3, yk330d2.3, yk160a6.3, yk320g4.5, yk177h11.3, yk187h11.5"

/codon_start=1

/product="Heat shock protein protein 4"

/protein_id="AAC71123.1"

/db_xref="GI:1947139"

/db_xref="WormBase:F43E2.8"

/translation="MKVFSLLIAFVANAYCDGASTEKEEKMTIGIDLTGYSCVGFNKGVEIANDQGNRIPTSVAFSGDQGERLIGDAKNQLTINPENTIFDAKRLI

SYLGHEKTVQDDIKHMPFKIVDKSNKPNVEVKVGSSETQFTPEVSAMVLTGMKQIAE

ERNILYVDGGFTFVSLTLTDSGVREVLATNGDTHLGGDFDQRMVEYFIKLYKKKS

GKDLKDNRAVKLRREVEKAKALSTQHQTKIEIESLFDGEDPSETLTAKFEELNM

DLFRATLQVQKVEDMDKVDHIEVLVGGSDRIPTKVQQLIKDFNGKEPGRGNGP

DEAVAYGAAYQAGVIGVENTGDVLLDVLNPLTIGETVGGVMTKLGIRNVTIPTKKS

QVFSTRAADSQSAVSIVIEGERPMWMDHKLGNFDVTGIPAPRGVQIEVTFEIDVN

GILHVSADGTGKNKLTITNDHNRSLSPEDIERMINDAKFAADDOAKQEKVESRNE

LEAVAYOMTKIADKKGKGLTDEKVSIESAVERAIEWLGNSQDASTENKEQKE

LESVVQPIVSKLSAGQGESEPESEHDEL"

/complement (3579. .6158)

/gene="F43E2.4"

/complement (join(3579. .3674,3729. .4145,4191. .4550,4599. .4925,4976. .5427,5478. .5597,5645. .6158))

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/standard_name="F43E2.4"

/notes="contains similarity to Pfam domains PF00664 (ABC transporter transmembrane region), PF00005 (ABC transporters); coded for by the following C. elegans cDNAs: yk3d1.3, yk3d1.5, yk12a6.3, yk12a6.5, yk155c4.5, yk287e1.5"

/codon_start=1

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/protein_id="AAC71121.1"

/db_xref="GI:1947137"

gene

CDS

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FOIFIRSFCAIAVLIIILNKRKVKVLPFVWICNAVYVSLIKELAFSEDSNQ
LYPLGWFVIMSLSGFTQVLVYFVFTSNFDRHLNLTAAENAGTSVTAAETV
RTEATSNVESGSSAPRALPHKVLRLLSYGHQWPFASGFVFLTVALARVETPN
YTAQISDINKRGIOALHSIIVLTLSATSLFGLRGKGFDAITAVTLRLIDL
FTSLRLQDIAFYIAVLVGTFTKAYSFYDKISKLOQTIAETNQMAEVSFVTRVRSF
MSRLAMVETIAVPLVGTFTKAYSFYDKISKLOQTIAETNQMAEVSFVTRVRSF
ACEKKELKFPEDRLSSTLSVNRKKSIAVLYFTWNEFCDNAIIIVAVFYGGHLMVTKG
MEKELITFLYQMOLGENLYLVSYMGLMEAVGASRKVFDLMNRKSPQFOLDGMQRP
FYNGNITSHVGTFTPSRPNPVLKDLTILSKSETVALVGPSSGKSSIVSLIEHFY
EPDEGSVLUDGPFKIDINHYHQRVALVQAQFVLVNGSVRHNILYGCDAFEDMLN
ASKMANVHDFVMELEKGYDTCGEGVQMGQKQRIARALVRNPVALILDEATSA
LQTESALVQQAQLSCAQBRTVIVAHRLSTIEKANKIAIVKGCILVQMGTHTEMLTD
TGMVYSLVSQMLSAKVGED"
8681. .9140
/gene="F43E2.9"
/join(8681. .8755,8967. .9140)
/gene="F43E2.9"
/standard_name="F43E2.9"
/notes="contains similarity to Clostridium acetobutylicum
Hypothetical protein CAC2790.; TR:Q97FF0"
/codon_start=1
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/protein_id="AAC71126.1"
/db_xref="GI:1947142"

gene

CDS

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Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 TGTGATTTTTCACAAAAA 358
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Db 25035 TGTGATTTTTCACAAAAA 25016
|||||

RESULT 13

CEC05A9/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CEC05A9 34309 bp DNA linear INV 03-DEC-2003
Caenorhabditis elegans cosmid C05A9, complete sequence.
270285
270285.1 GI:1235943
HTG; Ankyrin like; P-glycoprotein.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1

Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium
Science 282 (5396), 2012-2018 (1998)
99069613
9851916
The C. elegans Sequencing Consortium.
2 (bases 1 to 34309)
Kershaw, J.K.
Direct Submission

Submitted (22-MAR-1996) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.

Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.

For a graphical representation of this sequence and its analysis
see:- [http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?](http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=C05A9)
name=C05A9

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone C05A9. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C05A9 is at 1 in this sequence. The true right end of clone C05A9 is at 9694 in this sequence.

The true left end of clone T21E8 is at 34209 in this sequence. The true right end of clone F31B12 is at 14854 in this sequence. The start of this sequence (1..44) overlaps with the end of sequence CEF31B12.

The end of this sequence (34209..34309) overlaps with the start of sequence CBT21E8.

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FEATURES             source
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    /organism="Caenorhabditis elegans"
    /mol_type="genomic DNA"
    /strain="Bristol N2"
    /db_xref="taxon:6239"
    /clone="C05A9"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 341 TGATTTTTCACAAAAATA 360

Db 16743 TGATTTTTCACAAAAATA 16724

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RESULT 14
AL928690/c

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LOCUS             Mouse DNA sequence from clone RP23-443L19 on chromosome 2, complete
DEFINITION
ACCESSION             AL928690
VERSION             AL928690.9
KEYWORDS             HTG.
SOURCE             Mus musculus (house mouse)

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ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bates.K.
1 (bases 1 to 98535)

```

Direct Submission

```

Submitted (29-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

```

On Jan 30, 2003 this sequence version replaced gi:27817374. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information

on the WORMPEP database can be found at

http://www.sanger.ac.uk/projects/C_elegans/wormpep RP23-443L19 is

from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6.

FEATURES

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 476 GCGAAATCAGGAAGTGGGAT 495

Db 82173 GCGAAATCAGGAAGTGGGAT 82154

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RESULT 15
AC090524

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LOCUS             Caenorhabditis briggsae cosmid CB019H23, complete sequence.
DEFINITION
ACCESSION             AC090524
VERSION             AC090524.1
KEYWORDS             HTG.
SOURCE             Caenorhabditis briggsae

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ORGANISM

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 103244)

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The C. briggsae Genome Sequencing Center.

Unpublished

2 (bases 1 to 103244)

Waterston,R.

Direct Submission

Submitted (27-FEB-2001) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

Submitted by:

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA

e-mail: jspieth@watson.wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.

It may be shorter because we only sequence overlapping sections

once, or longer because we provide a small overlap between

neighboring submissions.

Location/Qualifiers

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAATAACA 363
|||
Db 58709 TTTTTCACAAAAATAACA 58728

Search completed: August 4, 2004, 15:11:03
Job time : 2199 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 13:24:02 ; Search time 304 Seconds
(without alignments)
6987.168 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcgc.....atcagggaagtggtatcgaaa 500

Scoring table: OLIGO_NUC

Gapop_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_29Jan04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002s.*

7: Geneseqn2003as.*

8: Geneseqn2003bs.*

9: Geneseqn2003cs.*

10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	500	100.0	500	6 ABQ73179	Abq73179 C. glutam
2	275	55.0	309400	5 AAH68534	Aah68534 C. glutam
3	134	26.8	1776	5 AAH68176	Aah68176 C. glutam
4	134	26.8	1776	7 ACA01190	Aca01190 C. glutam
5	112	22.4	1084	9 ADD13410	Add13410 C. glutam
6	100	20.0	1065	4 AAF71424	Aaf71424 Corynebact
7	23	4.6	579	3 AAC48302	Aac48302 Arabidops
8	23	4.6	580	3 AAC34575	Aac34575 Arabidops
9	19	3.8	497	8 ACH39788	Ach39788 Human foe
10	19	3.8	852	7 ABT42792	Abt42792 Human neu
11	19	3.8	6971	6 ABN80060	Abn80060 Human che
12	19	3.8	15373	6 ABL32467	Ab132467 Human imm
13	18	3.6	109	4 AAK58736	Aak58736 Human imm
14	18	3.6	487	9 ADE81992	Ade81992 Arabidops
15	18	3.6	584	8 ACH25364	Ach25364 Human adu
16	18	3.6	627	6 ABQ30138	Abq30138 Oligonuc1
17	18	3.6	627	6 ABQ30139	Abq30139 Oligonuc1
18	18	3.6	1068	6 ABN67095	Abn67095 Streptoco
19	18	3.6	1536	3 AAC42290	Aac42290 Arabidops
20	18	3.6	2000	7 ADA71674	Ada71674 Rice gene
21	18	3.6	2127	6 ABA93636	Aba93636 Human thy
22	18	3.6	2706	5 ABX71398	Abx71398 Human tra
23	18	3.6	2713	7 ADA53828	Ada53828 Human cod

24	18	3.6	2972	4 ABL29422	Ab129422 Drosophil
25	18	3.6	3201	4 ABL29420	Ab129420 Drosophil
26	18	3.6	6158	4 ABL02028	Ab102028 Drosophil
27	18	3.6	7309	9 ADB54292	Adb54292 Pretreat
28	18	3.6	14006	6 ABL33958	Ab133958 Human imm
29	18	3.6	15424	4 ABL29522	Ab129522 Drosophil
30	18	3.6	32313	4 AAK81578	Aak81578 Human imm
31	18	3.6	110000	6 ABN71527_09	Continuation (10 o
32	17	3.4	392	4 AAL24878	Aal24878 Human bre
33	17	3.4	513	8 ACH45236	Ach45236 Human foe
34	17	3.4	557	4 ABA59682	Aba59682 Human foe
35	17	3.4	557	4 AAI39547	Aai39547 Probe #82
36	17	3.4	557	4 AAK33821	Aak33821 Human bon
37	17	3.4	557	4 AAK07951	Aak07951 Human bra
38	17	3.4	557	4 ABS33631	Abs33631 Human liv
39	17	3.4	557	6 ABS08671	Abs08671 Human gen
40	17	3.4	569	4 AAI17081	Aai17081 Probe #70
41	17	3.4	569	4 ABA61415	Aba61415 Human foe
42	17	3.4	569	4 AAI41325	Aai41325 Probe #10
43	17	3.4	569	4 ABA29177	Aba29177 Probe #76
44	17	3.4	569	4 AAK35608	Aak35608 Human bon
45	17	3.4	569	4 AAK09715	Aak09715 Human bra
46	17	3.4	569	4 ABS35332	Abs35332 Human liv
47	17	3.4	569	6 ABS09905	Abs09905 Human gen
48	17	3.4	645	2 AAV37411	Aav37411 Streptoco
49	17	3.4	696	4 AAH90744	Aah90744 CFE 48 co
50	17	3.4	720	4 AAH90857	Aah90857 2CFE 48 c
51	17	3.4	744	7 ABX07371	Abx07371 S. pneumo
52	17	3.4	791	4 AAL25020	Aal25020 Human bre
53	17	3.4	965	9 ADE76303	Ade76303 Human BSK
54	17	3.4	1005	7 ACA43048	Aca43048 Prokaryot
55	17	3.4	1124	9 ADB69291	Adb69291 C. neofor
56	17	3.4	1170	7 ACA47870	Aca47870 Prokaryot
57	17	3.4	1243	2 AAV99106	Aav99106 DNA methy
58	17	3.4	1602	9 ADB87429	Adb87429 Transgene
59	17	3.4	2414	4 AAH15118	Aah15118 Human cDN
60	17	3.4	2546	2 AAX78320	Aax78320 A. chryso
61	17	3.4	2877	3 AAI10739	Aai10739 C. albica
62	17	3.4	3124	9 ADB68930	Adb68930 C. neofor
63	17	3.4	3128	5 AAS78582	Aas78582 DNA encod
64	17	3.4	3726	7 ABX08112	Abx08112 S. pneumo
65	17	3.4	3729	7 ACA49641	Aca49641 Prokaryot
66	17	3.4	4084	5 AAS71947	Aas71947 DNA encod
67	17	3.4	5092	4 AAI59458	Aai59458 Human pol
68	17	3.4	5290	4 ABL08212	Ab108212 Drosophil
69	17	3.4	5434	6 ABL62902	Ab162902 Breast ca
70	17	3.4	5434	6 ABL63111	Ab163111 Breast ca
71	17	3.4	5434	6 ABL64407	Ab164407 Stomach c
72	17	3.4	5434	7 ABT33842	Abt33842 DNMT1 cDN
73	17	3.4	5771	6 ABL33951	Ab133951 Human imm
74	17	3.4	5794	5 AAS78583	Aas78583 DNA encod
75	17	3.4	6069	9 ADD18703	Add18703 Human dis
76	17	3.4	7066	10 ADE77197	Ade77197 Human cDN
77	17	3.4	7514	7 ACC46596	Acc46596 Human dit
78	17	3.4	9905	6 ABL32062	Ab132062 Human imm
79	17	3.4	11443	2 AAV52182	Aav52182 Streptoco
80	17	3.4	19440	2 AAV99129	Aav99129 DNA methy
81	17	3.4	19553	4 ABK42538	Abk42538 Genomic s
82	17	3.4	19553	8 ADB60694	Adb60694 Connectiv
83	17	3.4	28473	2 AAV52216	Aav52216 Streptoco
84	17	3.4	35962	7 AB210104	Ab210104 Haematopo
85	17	3.4	96595	8 ADA02726	Ada02726 Human SYK
86	17	3.4	96595	9 ADB72464	Adb72464 Human SYK
87	17	3.4	110000	6 ABQ74964_1	Continuation (2 of
88	17	3.4	110000	7 ABS56454_14	Continuation (15 o
89	17	3.4	110000	7 ABS56454_18	Continuation (19 o
90	17	3.4	110000	7 ABS56454_20	Continuation (21 o
91	17	3.4	134525	2 AAQ04525	Aaq04525 Total bas
92	16	3.2	133	5 ABV56660	Abv56660 Human pro
93	16	3.2	146	6 ABK91750	Abk91750 DNA encod
94	16	3.2	185	4 AAS50733	Aas50733 Staphyloc
95	16	3.2	185	7 ACA18029	Aca18029 Prokaryot
96	16	3.2	210	7 ABX49361	Abx49361 Bovine ES

97	16	3.2	227	6	ABK79441	Abk79441 Bacillus	170	16	3.2	755	4	AAK75148	AAK75148 Human imm
98	16	3.2	238	3	AAC05174	Aac05174 Human sec	171	16	3.2	755	4	AAK75149	AAK75149 Human imm
99	16	3.2	246	4	AAS48802	Aas48802 Staphyloc	172	16	3.2	780	6	ABQ47385	Abq47385 Oligonuc1
100	16	3.2	246	4	AAS48821	Aas48821 Staphyloc	173	16	3.2	780	6	ABQ47384	Abq47384 Oligonuc1
101	16	3.2	246	4	AAS48821	Aas48821 Staphyloc	174	16	3.2	783	4	AAI95867	AAI95867 Human neu
102	16	3.2	246	4	AAS48883	Aas48883 Staphyloc	175	16	3.2	836	6	ABQ88749	Abq88749 Human pro
103	16	3.2	246	4	AAS48894	Aas48894 Staphyloc	176	16	3.2	844	6	ABQ88749	Abq88749 Human pro
104	16	3.2	246	4	AAS48894	Aas48894 Staphyloc	177	16	3.2	844	6	ABQ88749	Abq88749 Human pro
105	16	3.2	246	4	AAS48964	Aas48964 Staphyloc	178	16	3.2	845	6	ABQ82095	Abq82095 Rice meva
106	16	3.2	246	4	AAS48964	Aas48964 Staphyloc	179	16	3.2	852	3	AAK37746	AAK37746 Arabidops
107	16	3.2	246	4	ACA16070	Aca16070 Prokaryot	180	16	3.2	870	7	AAK37746	AAK37746 Arabidops
108	16	3.2	246	4	ACA16135	Aca16135 Prokaryot	181	16	3.2	896	9	ADC74842	Adc74842 Human pro
109	16	3.2	246	4	ACA16220	Aca16220 Prokaryot	182	16	3.2	901	7	ABZ52181	Abz52181 Aspergill
110	16	3.2	246	4	ACA16184	Aca16184 Prokaryot	183	16	3.2	911	3	AAK38429	AAK38429 Arabidops
111	16	3.2	246	4	ACA16094	Aca16094 Prokaryot	184	16	3.2	915	7	ACA28096	ACA28096 Prokaryot
112	16	3.2	247	7	ACA16064	Aca16064 Prokaryot	185	16	3.2	941	4	AAK64636	AAK64636 Human imm
113	16	3.2	247	7	ACA16145	Aca16145 Prokaryot	186	16	3.2	941	7	ABX63705	ABX63705 Human cDN
114	16	3.2	252	6	ABU77028	Abu77028 Human Ova	187	16	3.2	969	2	AAK61792	AAK61792 B. burgdo
115	16	3.2	267	6	ABU77263	Abu77263 Human ORF	188	16	3.2	984	4	ABU11599	ABU11599 Drosophil
116	16	3.2	300	2	AAZ12749	Aaz12749 Human gen	189	16	3.2	1005	2	AAZ22857	AAZ22857 Wheat ant
117	16	3.2	303	7	ACA39469	Aca39469 Prokaryot	190	16	3.2	1011	5	AAZ22857	AAZ22857 Wheat ant
118	16	3.2	307	3	AAC12495	Aac12495 Human sec	191	16	3.2	1011	5	AAZ22857	AAZ22857 Wheat ant
119	16	3.2	316	2	AAV87092	Aav87092 Bst clone	192	16	3.2	1037	3	AAZ22857	AAZ22857 Wheat ant
120	16	3.2	327	7	ABX53982	Abx53982 Bovine ES	193	16	3.2	1056	7	ACA18527	ACA18527 Prokaryot
121	16	3.2	334	3	AAA45074	Aaa45074 Human sec	194	16	3.2	1056	9	ADP78316	ADP78316 Endometri
122	16	3.2	378	4	AAI86260	Aai86260 Human pol	195	16	3.2	1065	7	ACC46280	ACC46280 Human dit
123	16	3.2	393	7	ACA30598	Aca30598 Prokaryot	196	16	3.2	1071	5	AAK67833	AAK67833 DNA encod
124	16	3.2	397	4	AAI84846	Aai84846 Human pol	197	16	3.2	1080	2	AAK61791	AAK61791 B. burgdo
125	16	3.2	429	7	ABX44906	Abx44906 Bovine ES	198	16	3.2	1110	9	ADC91989	ADC91989 E. faeciu
126	16	3.2	430	6	ABU65953	Abu65953 Lung canc	199	16	3.2	1134	4	AAI65118	AAI65118 Ribosomal
127	16	3.2	430	6	ABU65953	Abu65953 Lung canc	200	16	3.2	1400	3	ACC62024	ACC62024 Nucleotid
128	16	3.2	450	9	ADD32947	Add32947 Human mit	201	16	3.2	1410	8	ACC43044	ACC43044 Nucleotid
129	16	3.2	455	6	ACH376484	Ach376484 Human end	202	16	3.2	1410	8	ACC43044	ACC43044 Nucleotid
130	16	3.2	477	8	ACH32017	Ach32017 Human end	203	16	3.2	1410	8	ACC43044	ACC43044 Nucleotid
131	16	3.2	490	4	AAI16355	Aai16355 Probe #62	204	16	3.2	1434	6	AAU42886	AAU42886 Human DNA
132	16	3.2	490	4	ABA59201	Aba59201 Human foe	205	16	3.2	1458	7	ACA45761	ACA45761 Prokaryot
133	16	3.2	490	4	AAI38978	Aai38978 Probe #76	206	16	3.2	1531	7	ACC78321	ACC78321 DNA encod
134	16	3.2	490	4	ABA27960	Aba27960 Probe #64	207	16	3.2	1532	4	AAI93822	AAI93822 Human pol
135	16	3.2	490	4	AAK33180	Aak33180 Human bon	208	16	3.2	1539	9	ADC93278	ADC93278 E. faeciu
136	16	3.2	490	4	AAK07403	Aak07403 Human bra	209	16	3.2	1547	6	ABQ67092	Abq67092 Human col
137	16	3.2	490	4	ABQ32926	Abq32926 Human liv	210	16	3.2	1547	6	ABQ67092	Abq67092 Human col
138	16	3.2	490	6	ABS08008	Abs08008 Human gen	211	16	3.2	1547	6	ABQ67092	Abq67092 Human col
139	16	3.2	497	4	AAH71718	Aah71718 Human cer	212	16	3.2	1547	6	ABQ67092	Abq67092 Human col
140	16	3.2	497	4	AAH72541	Aah72541 Human cer	213	16	3.2	1559	2	AAI91855	AAI91855 Human bre
141	16	3.2	510	4	AAK85709	Aak85709 Human imm	214	16	3.2	1577	4	AAI91855	AAI91855 Human bre
142	16	3.2	510	4	AAK85710	Aak85710 Human imm	215	16	3.2	1584	7	ACA23970	ACA23970 Prokaryot
143	16	3.2	527	4	AAH70286	Aah70286 Human cer	216	16	3.2	1595	7	AAU51049	AAU51049 Human DME
144	16	3.2	549	7	ACD97652	Acd97652 Human col	217	16	3.2	1624	4	AAU51049	AAU51049 Human DME
145	16	3.2	554	4	ABA59800	Aba59800 Human foe	218	16	3.2	1638	7	ACA26091	ACA26091 Prokaryot
146	16	3.2	554	4	AAI39672	Aai39672 Probe #83	219	16	3.2	1657	5	ABV25742	ABV25742 Human pro
147	16	3.2	554	4	AAK33947	Aak33947 Human bon	220	16	3.2	1704	6	ACA33386	ACA33386 Prokaryot
148	16	3.2	554	4	AAK08073	Aak08073 Human liv	221	16	3.2	1763	7	ACA33386	ACA33386 Prokaryot
149	16	3.2	554	4	ABQ33752	Abq33752 Human bra	222	16	3.2	1804	4	AAU87114	AAU87114 NOV3 codi
150	16	3.2	554	6	ABS08758	Abs08758 Human gen	223	16	3.2	1827	6	ABN92451	ABN92451 Staphyloc
151	16	3.2	558	4	AAI17504	Aai17504 Probe #74	224	16	3.2	1896	9	ADC93359	ADC93359 E. faeciu
152	16	3.2	558	4	ABA62435	Aba62435 Human foe	225	16	3.2	1944	7	ADA53840	ADA53840 Human cod
153	16	3.2	558	4	AAK10777	Aak10777 Human bra	226	16	3.2	1956	7	ACA54394	ACA54394 Prokaryot
154	16	3.2	558	4	ABS36305	Abs36305 Human liv	227	16	3.2	2000	6	ABZ17051	ABZ17051 Arabidops
155	16	3.2	558	6	ABQ27674	Abq27674 Oligonuc1	228	16	3.2	2000	7	ADA69079	ADA69079 Arabidops
156	16	3.2	558	6	ABQ27675	Abq27675 Oligonuc1	229	16	3.2	2010	4	AAU57014	AAU57014 C. tracho
157	16	3.2	558	6	ABS10651	Abs10651 Human gen	230	16	3.2	2010	9	ADA42808	ADA42808 Chlamydia
158	16	3.2	626	6	AAU62848	Aau62848 Human G p	231	16	3.2	2011	4	AAU67113	AAU67113 Human cod
159	16	3.2	635	6	AAK31049	Aak31049 Plant dwa	232	16	3.2	2023	7	ADA53138	ADA53138 Human cod
160	16	3.2	656	6	ABK31043	Abk31043 Plant dwa	233	16	3.2	2026	7	ACC78319	ACC78319 DNA encod
161	16	3.2	675	7	ACA36670	Aca36670 Prokaryot	234	16	3.2	2089	7	ACC78320	ACC78320 DNA encod
162	16	3.2	690	7	ACF74295	Acf74295 Staphyloc	235	16	3.2	2177	9	ABT07590	ABT07590 Human bre
163	16	3.2	708	6	ABQ68488	Abq68488 Listeria	236	16	3.2	2177	9	ABT07590	ABT07590 Human bre
164	16	3.2	714	8	ADB81693	Adb81693 Human cDN	237	16	3.2	2196	3	AAU72428	AAU72428 Human nuc
165	16	3.2	715	3	AAU44749	Aau44749 Zea mays	238	16	3.2	2237	6	ABX91964	ABX91964 Lung spec
166	16	3.2	729	6	ABL92707	AbL92707 Chlamydia	239	16	3.2	2237	6	ABX91964	ABX91964 Lung spec
167	16	3.2	734	3	AAU48563	Aau48563 Arabidops	240	16	3.2	2340	4	AAU54405	AAU54405 Primer #8
168	16	3.2	736	3	AAU34369	Aau34369 Arabidops	241	16	3.2	2340	4	AAU54405	AAU54405 Primer #8
169	16	3.2	745	4	AAU23230	Aau23230 Human bre	242	16	3.2	2340	4	AAU54405	AAU54405 Primer #8

C 243	16	3.2	2340	7	ACA75666	ACA75666 Novel hum	C 316	16	3.2	2340	7	ACA73244	ACA73244 Novel hum
C 244	16	3.2	2340	7	ACA71146	ACA71146 Human sec	C 317	16	3.2	2340	7	ACA68787	ACA68787 Novel hum
C 245	16	3.2	2340	7	ACC87674	ACC87674 Human sec	C 318	16	3.2	2340	7	ACA74631	ACA74631 cDNA enco
C 246	16	3.2	2340	7	ACC87060	ACC87060 Human sec	C 319	16	3.2	2340	7	ACA70498	ACA70498 Human sec
C 247	16	3.2	2340	7	ACD04233	ACD04233 Human sec	C 320	16	3.2	2340	7	ACD14684	ACD14684 Human PRO
C 248	16	3.2	2340	7	ACA69564	ACA69564 cDNA enco	C 321	16	3.2	2340	7	ACA68356	ACA68356 Novel hum
C 249	16	3.2	2340	7	ACA90409	ACA90409 Novel hum	C 322	16	3.2	2340	7	ABX98821	ABX98821 Novel hum
C 250	16	3.2	2340	7	ACC89516	ACC89516 Human sec	C 323	16	3.2	2340	7	ACC81298	ACC81298 Human sec
C 251	16	3.2	2340	7	ACA98307	ACA98307 Novel hum	C 324	16	3.2	2340	7	ACA95622	ACA95622 Novel hum
C 252	16	3.2	2340	7	ACA93949	ACA93949 Human sec	C 325	16	3.2	2340	7	ACD04540	ACD04540 Novel hum
C 253	16	3.2	2340	7	ACD15342	ACD15342 Human sec	C 326	16	3.2	2340	7	ACC87981	ACC87981 Human sec
C 254	16	3.2	2340	7	ACD08929	ACD08929 Human sec	C 327	16	3.2	2340	7	ACF12643	ACF12643 Human sec
C 255	16	3.2	2340	7	ACC96849	ACC96849 Human sec	C 328	16	3.2	2340	7	ACA96358	ACA96358 Human PRO
C 256	16	3.2	2340	7	ACF15570	ACF15570 Human sec	C 329	16	3.2	2340	7	ACA65132	ACA65132 Human PRO
C 257	16	3.2	2340	7	ACA72937	ACA72937 Human PRO	C 330	16	3.2	2340	7	ACA73858	ACA73858 Human sec
C 258	16	3.2	2340	7	ACD03109	ACD03109 Novel hum	C 331	16	3.2	2340	7	ACA74270	ACA74270 Novel hum
C 259	16	3.2	2340	7	ACD01924	ACD01924 Novel hum	C 332	16	3.2	2340	7	ACA96665	ACA96665 Human PRO
C 260	16	3.2	2340	7	ACA92116	ACA92116 Novel hum	C 333	16	3.2	2340	7	ACD10771	ACD10771 cDNA enco
C 261	16	3.2	2340	7	ACA89541	ACA89541 cDNA enco	C 334	16	3.2	2340	7	ACC91467	ACC91467 Human sec
C 262	16	3.2	2340	7	ACA73551	ACA73551 Human sec	C 335	16	3.2	2340	7	ACD02802	ACD02802 cDNA enco
C 263	16	3.2	2340	7	ACA05866	ACA05866 Human sec	C 336	16	3.2	2340	7	ACC87367	ACC87367 Human sec
C 264	16	3.2	2340	7	ACA66700	ACA66700 cDNA enco	C 337	16	3.2	2340	7	ACC85951	ACC85951 Human sec
C 265	16	3.2	2340	7	ACF20275	ACF20275 Human sec	C 338	16	3.2	2340	7	ACA65439	ACA65439 Human PRO
C 266	16	3.2	2340	7	ACF19661	ACF19661 Human sec	C 339	16	3.2	2340	7	ACA94256	ACA94256 Human sec
C 267	16	3.2	2340	7	ACD21949	ACD21949 Human sec	C 340	16	3.2	2340	7	ACA98000	ACA98000 Human PRO
C 268	16	3.2	2340	7	ACF13114	ACF13114 Human sec	C 341	16	3.2	2340	7	ACA91502	ACA91502 Novel hum
C 269	16	3.2	2340	7	ACD25217	ACD25217 Human sec	C 342	16	3.2	2340	7	ACA90716	ACA90716 Novel hum
C 270	16	3.2	2340	7	ACF00266	ACF00266 Human sec	C 343	16	3.2	2340	7	ACD16263	ACD16263 Human sec
C 271	16	3.2	2340	7	ACA72323	ACA72323 Novel hum	C 344	16	3.2	2340	7	ACD17424	ACD17424 Human sec
C 272	16	3.2	2340	7	ACD04847	ACD04847 Novel hum	C 345	16	3.2	2340	7	ACC92081	ACC92081 Human sec
C 273	16	3.2	2340	7	ACD18308	ACD18308 Human sec	C 346	16	3.2	2340	7	ACA74938	ACA74938 cDNA enco
C 274	16	3.2	2340	7	ACD08315	ACD08315 Human sec	C 347	16	3.2	2340	7	ACA91809	ACA91809 Human PRO
C 275	16	3.2	2340	7	ACA88749	ACA88749 Novel hum	C 348	16	3.2	2340	7	ACA71453	ACA71453 Human sec
C 276	16	3.2	2340	7	ACA70191	ACA70191 Human sec	C 349	16	3.2	2340	7	ACC90853	ACC90853 Human sec
C 277	16	3.2	2340	7	ACD12413	ACD12413 Novel hum	C 350	16	3.2	2340	7	ACA65863	ACA65863 cDNA enco
C 278	16	3.2	2340	7	ACC74328	ACC74328 Human sec	C 351	16	3.2	2340	7	ACA95008	ACA95008 cDNA enco
C 279	16	3.2	2340	7	ACD15956	ACD15956 Human sec	C 352	16	3.2	2340	7	ACD16570	ACD16570 Human sec
C 280	16	3.2	2340	7	ACD25524	ACD25524 Novel hum	C 353	16	3.2	2340	7	ACD15649	ACD15649 Human sec
C 281	16	3.2	2340	7	ACD18001	ACD18001 Human sec	C 354	16	3.2	2340	7	ABX16752	ABX16752 Human CDN
C 282	16	3.2	2340	7	ACC88288	ACC88288 Human sec	C 355	16	3.2	2340	8	ACA97693	ACA97693 Human PRO
C 283	16	3.2	2340	7	ACD21642	ACD21642 Human sec	C 356	16	3.2	2340	8	ACA99142	ACA99142 Novel hum
C 284	16	3.2	2340	7	ACD18709	ACD18709 Human sec	C 357	16	3.2	2340	8	ACC91774	ACC91774 Human sec
C 285	16	3.2	2340	7	ABX98319	ABX98319 Human CDN	C 358	16	3.2	2340	8	ACD11185	ACD11185 Novel hum
C 286	16	3.2	2340	7	ACD14070	ACD14070 Human PRO	C 359	16	3.2	2340	8	ACD15035	ACD15035 Human sec
C 287	16	3.2	2340	7	ACD09850	ACD09850 Human sec	C 360	16	3.2	2340	8	ACD11799	ACD11799 Human sec
C 288	16	3.2	2340	7	ACC88595	ACC88595 Human sec	C 361	16	3.2	2340	8	ACC95928	ACC95928 Human sec
C 289	16	3.2	2340	7	ACD21335	ACD21335 Human sec	C 362	16	3.2	2340	8	ACF16491	ACF16491 Human sec
C 290	16	3.2	2340	7	ABX75707	ABX75707 Human CDN	C 363	16	3.2	2340	8	ACF02609	ACF02609 Human sec
C 291	16	3.2	2340	7	ABX97910	ABX97910 Human PRO	C 364	16	3.2	2340	8	ACF21503	ACF21503 Human sec
C 292	16	3.2	2340	7	ACA97386	ACA97386 Novel hum	C 365	16	3.2	2340	8	ACF210187	ACF210187 Human sec
C 293	16	3.2	2340	7	ACA57849	ACA57849 Human PRO	C 366	16	3.2	2340	8	ACF78080	ACF78080 Human sec
C 294	16	3.2	2340	7	ACD14377	ACD14377 Human sec	C 367	16	3.2	2340	8	ACD46785	ACD46785 Human sec
C 295	16	3.2	2340	7	ACC91160	ACC91160 Human sec	C 368	16	3.2	2340	8	ACD49548	ACD49548 Human sec
C 296	16	3.2	2340	7	ACC88902	ACC88902 Human sec	C 369	16	3.2	2340	8	ACD28315	ACD28315 Human sec
C 297	16	3.2	2340	7	ACD07099	ACD07099 Human PRO	C 370	16	3.2	2340	8	ACF28315	ACF28315 Human sec
C 298	16	3.2	2340	7	ACA67550	ACA67550 Human PRO	C 371	16	3.2	2340	8	ACC89005	ACC89005 Human sec
C 299	16	3.2	2340	7	ACC81605	ACC81605 Human sec	C 372	16	3.2	2340	8	ACD84400	ACD84400 Human PRO
C 300	16	3.2	2340	7	ACC89209	ACC89209 Human sec	C 373	16	3.2	2340	8	ACD99174	ACD99174 cDNA enco
C 301	16	3.2	2340	7	ACC86565	ACC86565 Human sec	C 374	16	3.2	2340	8	ADA78085	ADA78085 Human sec
C 302	16	3.2	2340	7	ACC98823	ACC98823 Human sec	C 375	16	3.2	2340	8	ACF48916	ACF48916 Human sec
C 303	16	3.2	2340	7	ACC93002	ACC93002 Human sec	C 376	16	3.2	2340	8	ACD09236	ACD09236 Human sec
C 304	16	3.2	2340	7	ACA72630	ACA72630 Human PRO	C 377	16	3.2	2340	8	ACF12029	ACF12029 Human sec
C 305	16	3.2	2340	7	ACA89148	ACA89148 Human PRO	C 378	16	3.2	2340	8	ACF41263	ACF41263 Human sec
C 306	16	3.2	2340	7	ACA69884	ACA69884 Human sec	C 379	16	3.2	2340	8	ACF15877	ACF15877 Human sec
C 307	16	3.2	2340	7	ACA97027	ACA97027 Novel hum	C 380	16	3.2	2340	8	ACF16184	ACF16184 Human sec
C 308	16	3.2	2340	7	ACA91023	ACA91023 Novel hum	C 381	16	3.2	2340	8	ACD32011	ACD32011 Human sec
C 309	16	3.2	2340	7	ACA70805	ACA70805 Human sec	C 382	16	3.2	2340	8	ACF18819	ACF18819 Human sec
C 310	16	3.2	2340	7	ACA95315	ACA95315 Novel hum	C 383	16	3.2	2340	8	ACF09266	ACF09266 Human sec
C 311	16	3.2	2340	7	ACC86258	ACC86258 Human sec	C 384	16	3.2	2340	8	ACF78387	ACF78387 Human sec
C 312	16	3.2	2340	7	ACC90130	ACC90130 Human sec	C 385	16	3.2	2340	8	ACF51986	ACF51986 Human sec
C 313	16	3.2	2340	7	ACD12738	ACD12738 Human sec	C 386	16	3.2	2340	8	ACF26473	ACF26473 Human sec
C 314	16	3.2	2340	7	ACF19968	ACF19968 Human PRO	C 387	16	3.2	2340	8	ACF24266	ACF24266 Human sec
C 315	16	3.2	2340	7	ABX76912	ABX76912 Human PRO	C 388	16	3.2	2340	8	ACF63577	ACF63577 Human sec

C 389	16	3.2	2340	8	ACF50451	Human	sec	AcF50451	Human	sec	C 462	16	3.2	2340	8	ACF60217	Human	sec
C 390	16	3.2	2340	8	ACH07922	Human	sec	Ach07922	Human	sec	C 463	16	3.2	2340	8	ACF46767	Human	sec
C 391	16	3.2	2340	8	ACF13728	Human	sec	Acf13728	Human	sec	C 464	16	3.2	2340	8	ACF75624	Human	sec
C 392	16	3.2	2340	8	ACD41654	Human	sec	Acd41654	Human	sec	C 465	16	3.2	2340	8	ADA79877	Human	sec
C 393	16	3.2	2340	8	ACF32067	Human	sec	Acf32067	Human	sec	C 466	16	3.2	2340	8	ACF17284	Human	sec
C 394	16	3.2	2340	8	ACF23345	Human	sec	Acf23345	Human	sec	C 467	16	3.2	2340	8	ACF23038	Human	sec
C 395	16	3.2	2340	8	ACF40035	Human	sec	Acf40035	Human	sec	C 468	16	3.2	2340	8	ACF08038	Human	sec
C 396	16	3.2	2340	8	ACD45557	Human	sec	Acd45557	Human	sec	C 469	16	3.2	2340	8	ACF08345	Human	sec
C 397	16	3.2	2340	8	ACD53214	Human	sec	Acf53214	Human	sec	C 470	16	3.2	2340	8	ACF53828	Human	sec
C 398	16	3.2	2340	8	ACF27394	Human	sec	Acf27394	Human	sec	C 471	16	3.2	2340	8	ACF53828	Human	sec
C 399	16	3.2	2340	8	ACF45232	Human	sec	Acf45232	Human	sec	C 472	16	3.2	2340	8	ACD47092	Human	sec
C 400	16	3.2	2340	8	ACF29850	Human	sec	Acf29850	Human	sec	C 473	16	3.2	2340	8	ACF47381	Human	sec
C 401	16	3.2	2340	8	ACD89926	Human	sec	Acd89926	Human	sec	C 474	16	3.2	2340	8	ACF46153	Human	sec
C 402	16	3.2	2340	8	ACD84707	Human	PRO	Acd84707	Human	PRO	C 475	16	3.2	2340	8	ACD86242	Human	sec
C 403	16	3.2	2340	8	ACD98867	cdNA	enco	ACd98867	cdNA	enco	C 476	16	3.2	2340	8	ACF52600	Human	sec
C 404	16	3.2	2340	8	ACF77159	Human	sec	Acf77159	Human	sec	C 477	16	3.2	2340	8	ACF52907	Human	sec
C 405	16	3.2	2340	8	ACF76852	Human	sec	Acf76852	Human	sec	C 478	16	3.2	2340	8	ACF64900	Human	sec
C 406	16	3.2	2340	8	ACF49837	Human	sec	Acf49837	Human	sec	C 479	16	3.2	2340	8	ACF76545	Human	sec
C 407	16	3.2	2340	8	ACF50144	Human	sec	Acf50144	Human	sec	C 480	16	3.2	2340	8	ACF61445	Human	sec
C 408	16	3.2	2340	8	ACD09543	Human	sec	Acd09543	Human	sec	C 481	16	3.2	2340	8	ACF61752	Human	sec
C 409	16	3.2	2340	8	ACD08622	Human	sec	Acd08622	Human	sec	C 482	16	3.2	2340	8	ACF61752	Human	sec
C 410	16	3.2	2340	8	ACF12336	Human	sec	Acf12336	Human	sec	C 483	16	3.2	2340	8	ACD30783	Human	sec
C 411	16	3.2	2340	8	ACC94844	Human	sec	Acc94844	Human	sec	C 484	16	3.2	2340	8	ACD31704	Human	sec
C 412	16	3.2	2340	8	ACD22563	Human	sec	Acd22563	Human	sec	C 485	16	3.2	2340	8	ACD32625	Human	sec
C 413	16	3.2	2340	8	ACF15263	Human	sec	Acf15263	Human	sec	C 486	16	3.2	2340	8	ACF17591	Human	sec
C 414	16	3.2	2340	8	ACC97358	Human	sec	Acc97358	Human	sec	C 487	16	3.2	2340	8	ACF07424	Human	sec
C 415	16	3.2	2340	8	ACC92388	Human	sec	Acc92388	Human	sec	C 488	16	3.2	2340	8	ACF20582	Human	sec
C 416	16	3.2	2340	8	ACF14035	Human	sec	Acf14035	Human	sec	C 489	16	3.2	2340	8	ACF20889	Human	sec
C 417	16	3.2	2340	8	ACF14342	Human	sec	Acf14342	Human	sec	C 490	16	3.2	2340	8	ACF21196	Human	sec
C 418	16	3.2	2340	8	ACF09573	Human	sec	Acf09573	Human	sec	C 491	16	3.2	2340	8	ACD47706	Human	sec
C 419	16	3.2	2340	8	ACD68444	Novel	hum	Acd68444	Novel	hum	C 492	16	3.2	2340	8	ACF47688	Human	sec
C 420	16	3.2	2340	8	ACD45864	Human	sec	Acd45864	Human	sec	C 493	16	3.2	2340	8	ACF53521	Human	sec
C 421	16	3.2	2340	8	ACD48013	Human	sec	Acd48013	Human	sec	C 494	16	3.2	2340	8	ACD86856	Human	sec
C 422	16	3.2	2340	8	ACD67744	cdNA	enco	ACd67744	cdNA	enco	C 495	16	3.2	2340	8	ACH05104	cdNA	enco
C 423	16	3.2	2340	8	ACF25552	Human	sec	Acf25552	Human	sec	C 496	16	3.2	2340	8	ACF44601	Human	sec
C 424	16	3.2	2340	8	ACF29236	Human	sec	Acf29236	Human	sec	C 497	16	3.2	2340	8	ADA81604	Human	sec
C 425	16	3.2	2340	8	ACD85014	Human	sec	Acd85014	Human	sec	C 498	16	3.2	2340	8	ACD22256	Human	sec
C 426	16	3.2	2340	8	ACD84093	Human	PRO	Acd84093	Human	PRO	C 499	16	3.2	2340	8	ACD24603	Human	sec
C 427	16	3.2	2340	8	ACD88084	Human	sec	Acd88084	Human	sec	C 500	16	3.2	2340	8	ACD39806	cdNA	enco
C 428	16	3.2	2340	8	ACF30771	Human	sec	Acf30771	Human	sec	C 501	16	3.2	2340	8	ACD40113	cdNA	enco
C 429	16	3.2	2340	8	ACF32374	Human	sec	Acf32374	Human	sec	C 502	16	3.2	2340	8	ACF13421	Human	sec
C 430	16	3.2	2340	8	ACH12034	cdNA	enco	Ach12034	cdNA	enco	C 503	16	3.2	2340	8	ACF03223	Human	sec
C 431	16	3.2	2340	8	ACH12341	cdNA	enco	Ach12341	cdNA	enco	C 504	16	3.2	2340	8	ACF78694	Human	sec
C 432	16	3.2	2340	8	ACD40733	Human	sec	Acd40733	Human	sec	C 505	16	3.2	2340	8	ACF11415	Human	sec
C 433	16	3.2	2340	8	ACF18205	Human	sec	Acf18205	Human	sec	C 506	16	3.2	2340	8	ACF50758	Human	sec
C 434	16	3.2	2340	8	ACF08652	Human	sec	Acf08652	Human	sec	C 507	16	3.2	2340	8	ACF34253	Human	sec
C 435	16	3.2	2340	8	ACF311453	Human	sec	Acf311453	Human	sec	C 508	16	3.2	2340	8	ACD46478	Human	sec
C 436	16	3.2	2340	8	ACF52293	Human	sec	Acf52293	Human	sec	C 509	16	3.2	2340	8	ACD48320	Human	sec
C 437	16	3.2	2340	8	ACD50162	Human	sec	Acd50162	Human	sec	C 510	16	3.2	2340	8	ACF27701	Human	sec
C 438	16	3.2	2340	8	ACF38865	Human	sec	Acf38865	Human	sec	C 511	16	3.2	2340	8	ACF24573	Human	sec
C 439	16	3.2	2340	8	ACF26780	Human	sec	Acf26780	Human	sec	C 512	16	3.2	2340	8	ACD85628	Human	sec
C 440	16	3.2	2340	8	ACF24880	Human	sec	Acf24880	Human	sec	C 513	16	3.2	2340	8	ACD90233	Human	PRO
C 441	16	3.2	2340	8	ACF46460	Human	sec	Acf46460	Human	sec	C 514	16	3.2	2340	8	ACD83786	Human	PRO
C 442	16	3.2	2340	8	ACF28008	Human	sec	Acf28008	Human	sec	C 515	16	3.2	2340	8	ACF49223	Human	sec
C 443	16	3.2	2340	8	ACD89312	Human	sec	Acd89312	Human	sec	C 516	16	3.2	2340	8	ACH07308	Human	sec
C 444	16	3.2	2340	8	ACF63884	Human	sec	Acf63884	Human	sec	C 517	16	3.2	2340	8	ACH07615	Human	sec
C 445	16	3.2	2340	8	ACF60524	Human	sec	Acf60524	Human	sec	C 518	16	3.2	2340	8	ACH08229	Human	sec
C 446	16	3.2	2340	8	ACH12648	cdNA	enco	Ach12648	cdNA	enco	C 519	16	3.2	2340	8	ACH11420	cdNA	enco
C 447	16	3.2	2340	8	ACH10071	Human	sec	Ach10071	Human	sec	C 520	16	3.2	2340	8	ACH11727	cdNA	enco
C 448	16	3.2	2340	8	ACD03926	Human	sec	Acd03926	Human	sec	C 521	16	3.2	2340	8	ACH10378	Human	sec
C 449	16	3.2	2340	8	ACD10464	Human	sec	Acd10464	Human	sec	C 522	16	3.2	2340	8	ACF01381	Human	sec
C 450	16	3.2	2340	8	ACD12106	Human	sec	Acd12106	Human	sec	C 523	16	3.2	2340	8	ACF40956	Human	sec
C 451	16	3.2	2340	8	ACF42491	Human	sec	Acf42491	Human	sec	C 524	16	3.2	2340	8	ACD24296	Human	sec
C 452	16	3.2	2340	8	ACF18512	Human	sec	Acf18512	Human	sec	C 525	16	3.2	2340	8	ACD31397	Human	sec
C 453	16	3.2	2340	8	ACF02302	Human	sec	Acf02302	Human	sec	C 526	16	3.2	2340	8	ACD31789	Human	sec
C 454	16	3.2	2340	8	ACF21810	Human	sec	Acf21810	Human	sec	C 527	16	3.2	2340	8	ACF32681	Human	sec
C 455	16	3.2	2340	8	ACF10494	Human	sec	Acf10494	Human	sec	C 528	16	3.2	2340	8	ACF40342	Human	sec
C 456	16	3.2	2340	8	ACF33946	Human	sec	Acf33946	Human	sec	C 529	16	3.2	2340	8	ACF48302	Human	sec
C 457	16	3.2	2340	8	ACF44908	Human	sec	Acf44908	Human	sec	C 530	16	3.2	2340	8	ACF38251	Human	sec
C 458	16	3.2	2340	8	ACD90540	Human	sec	Acd90540	Human	sec	C 531	16	3.2	2340	8	ACF25187	Human	sec
C 459	16	3.2	2340	8	ACD91153	Human	sec	Acd91153	Human	sec	C 532	16	3.2	2340	8	ACF27087	Human	sec
C 460	16	3.2	2340	8	ACF30464	Human	sec	Acf30464	Human	sec	C 533	16	3.2	2340	8	ACF29543	Human	sec
C 461	16	3.2	2340	8	ACD87163	Human	sec	Acd87163	Human	sec	C 534	16	3.2	2340	8	ACD87777	Human	sec

535	16	3.2	2340	8	ACF76238	Human sec	ACf76238	Human sec	8	ACF08959	Human sec
536	16	3.2	2340	8	ACF49530	Human sec	ACf49530	Human sec	8	ACF33295	Human sec
537	16	3.2	2340	8	ACF43987	Human sec	ACf43987	Human sec	8	ACF54749	Human sec
538	16	3.2	2340	8	ACH06332	cDNA enco	Ach06332	cDNA enco	8	ACf48609	Human sec
539	16	3.2	2340	8	ACH06639	cDNA enco	Ach06639	cDNA enco	8	ACD47399	Human sec
540	16	3.2	2340	8	ADA83402	Human sec	Ada83402	Human sec	8	ACD49241	Human sec
541	16	3.2	2340	8	ACC92695	Human sec	Acc92695	Human sec	8	ACf37944	Human sec
542	16	3.2	2340	8	ACC93309	Human sec	Acc93309	Human sec	8	ACF30157	Human sec
543	16	3.2	2340	8	ACF19354	Human sec	ACf19354	Human sec	8	ACD87470	Human sec
544	16	3.2	2340	8	ACD13045	Human sec	ACd13045	Human sec	8	ACF62059	Human sec
545	16	3.2	2340	8	ACF06503	Human sec	ACf06503	Human sec	8	ACH10992	Human sec
546	16	3.2	2340	8	ACC94537	Human sec	Acc94537	Human sec	8	ACH10157	Human sec
547	16	3.2	2340	8	ACC97965	Human sec	Acc97965	Human sec	8	ACD16882	cDNA enco
548	16	3.2	2340	8	ACC94230	Human sec	Acc94230	Human sec	8	ACC99179	Human sec
549	16	3.2	2340	8	ACF42184	Human sec	ACf42184	Human sec	8	ACF00573	Human sec
550	16	3.2	2340	8	ACD31090	Human sec	ACd31090	Human sec	8	ACD41040	Human sec
551	16	3.2	2340	8	ACD43119	cDNA enco	ACd43119	cDNA enco	8	ACF14649	Human sec
552	16	3.2	2340	8	ACD43426	cDNA enco	ACd43426	cDNA enco	8	ACF22424	Human sec
553	16	3.2	2340	8	ACF14956	Human sec	ACf14956	Human sec	8	ACF79001	Human sec
554	16	3.2	2340	8	ACF01688	Human sec	ACf01688	Human sec	8	ACD68090	Novel hum
555	16	3.2	2340	8	ACF31760	Human sec	ACf31760	Human sec	8	ACF11722	Human sec
556	16	3.2	2340	8	ACD67437	cDNA enco	ACd67437	cDNA enco	8	ACF51679	Human sec
557	16	3.2	2340	8	ACD48627	Human sec	ACd48627	Human sec	8	ACF33602	Human sec
558	16	3.2	2340	8	ACD48934	Human sec	ACd48934	Human sec	8	ACD49855	Human sec
559	16	3.2	2340	8	ACF511372	Human sec	ACf511372	Human sec	8	ACF37637	Human sec
560	16	3.2	2340	8	ACF54135	Human sec	ACf54135	Human sec	8	ACD28622	Human sec
561	16	3.2	2340	8	ACF525859	Human sec	ACf525859	Human sec	8	ACD88698	Human sec
562	16	3.2	2340	8	ACF39172	Human sec	ACf39172	Human sec	8	ACF75317	Human sec
563	16	3.2	2340	8	ACF28929	Human sec	ACf28929	Human sec	8	ACF61138	Human sec
564	16	3.2	2340	8	ACD90846	Human sec	ACd90846	Human sec	8	ACF44294	Human sec
565	16	3.2	2340	8	ACD86549	Human sec	ACd86549	Human sec	8	ACH08536	Human sec
566	16	3.2	2340	8	ACH05411	cDNA enco	Ach05411	cDNA enco	8	ACC93923	Human sec
567	16	3.2	2340	8	ACF65207	Human sec	ACf65207	Human sec	8	ACD21028	Human sec
568	16	3.2	2340	8	ADB20445	Human sec	ADB20445	Human sec	8	ACF06810	Human sec
569	16	3.2	2340	8	ACF433680	Human sec	ACf433680	Human sec	8	ACD20721	Human sec
570	16	3.2	2340	8	ACH09150	Human sec	ACH09150	Human sec	8	ACD22870	Human sec
571	16	3.2	2340	8	ACH09457	Human sec	ACH09457	Human sec	8	ACF41570	Human sec
572	16	3.2	2340	8	ADA78697	Human sec	Ada78697	Human sec	8	ACF07117	Human sec
573	16	3.2	2340	8	ACF09880	Human sec	ACf09880	Human sec	8	ACF77773	Human sec
574	16	3.2	2340	8	ACF51065	Human sec	ACf51065	Human sec	8	ACD46171	Human sec
575	16	3.2	2340	8	ACF23959	Human sec	ACf23959	Human sec	8	ACF47074	Human sec
576	16	3.2	2340	8	ACH088391	Human sec	ACH088391	Human sec	8	ACF54442	Human sec
577	16	3.2	2340	8	ACH09764	Human sec	ACH09764	Human sec	8	ACF45846	Human sec
578	16	3.2	2340	8	ACH10685	Human sec	ACH10685	Human sec	8	ACF45539	Human sec
579	16	3.2	2340	8	ACH11492	Human sec	ACH11492	Human sec	8	ACF38558	Human sec
580	16	3.2	2340	8	ACC96542	Human sec	ACC96542	Human sec	8	ACF89619	Human sec
581	16	3.2	2340	8	ACH04546	Human cDN	Ach04546	Human cDN	8	ACD85321	Human sec
582	16	3.2	2340	8	ACC98572	Human sec	ACC98572	Human sec	8	ACD85935	Human sec
583	16	3.2	2340	8	ACF41877	Human sec	ACf41877	Human sec	8	ACF75931	Human sec
584	16	3.2	2340	8	ACF16798	Human sec	ACf16798	Human sec	8	ACH05718	cDNA enco
585	16	3.2	2340	8	ACD32318	Human sec	ACd32318	Human sec	8	ACH05718	cDNA enco
586	16	3.2	2340	8	ACD30476	Human sec	ACd30476	Human sec	8	ADa82768	Human sec
587	16	3.2	2340	8	ACD41347	Human sec	ACd41347	Human sec	8	ACF55977	Human sec
588	16	3.2	2340	8	ACF07731	Human sec	ACf07731	Human sec	8	ACF55363	Human sec
589	16	3.2	2340	8	ACF31146	Human sec	ACf31146	Human sec	8	ADb86076	Human sec
590	16	3.2	2340	8	ACF77466	Human sec	ACf77466	Human sec	8	ACF56284	Human sec
591	16	3.2	2340	8	ACF11108	Human sec	ACf11108	Human sec	8	ACF56591	Human sec
592	16	3.2	2340	8	ACF32988	Human sec	ACf32988	Human sec	8	ACF55670	Human sec
593	16	3.2	2340	8	ACF26166	Human sec	ACf26166	Human sec	8	ACF55056	Human sec
594	16	3.2	2340	8	ACD83479	Human PRO	ACD83479	Human PRO	8	ADc18155	Human PRO
595	16	3.2	2340	8	ACF23652	Human sec	ACf23652	Human sec	8	ADd05806	Human sec
596	16	3.2	2340	8	ACF43066	Human sec	ACf43066	Human sec	8	ADd70801	Human cDN
597	16	3.2	2340	8	ACF43373	Human sec	ACf43373	Human sec	8	ADd70801	Human cDN
598	16	3.2	2340	8	ACH06025	cDNA enco	Ach06025	cDNA enco	8	ADd70801	Human cDN
599	16	3.2	2340	8	ACH08843	Human sec	ACH08843	Human sec	8	ADd70324	Human cDN
600	16	3.2	2340	8	ACC90437	Human sec	ACC90437	Human sec	8	ADd38445	Human cDN
601	16	3.2	2340	8	ACF10801	Human sec	ACf10801	Human sec	8	ADd38445	Human cDN
602	16	3.2	2340	8	ACC93616	Human sec	ACC93616	Human sec	8	ADd38924	Human cDN
603	16	3.2	2340	8	ACC96235	Human sec	ACC96235	Human sec	8	ADd40355	Human cDN
604	16	3.2	2340	8	ACD24910	Human sec	ACd24910	Human sec	8	ADe50576	Human cDN
605	16	3.2	2340	8	ACF01395	Human sec	ACf01395	Human sec	8	ADe20188	Human cDN
606	16	3.2	2340	8	ACF22117	Human sec	ACf22117	Human sec	8	ADe50099	Human cDN
607	16	3.2	2340	8	ACF22731	Human sec	ACf22731	Human sec	8	ADe21657	Human cDN
									10	ADe74470	Human sec

C 681	16	3.2	2340	10	ADE75082	Human sec	Ade75082	C 754	16	3.2	6478	9	ADB54155	Pretreat
C 682	16	3.2	2346	2	AAV42000	Nucleotid	Nuc42000	C 755	16	3.2	6478	9	ADB54283	Pretreat
C 683	16	3.2	2346	2	AAV93832	A. hydrop	Ahy93832	C 756	16	3.2	6591	4	AAS46283	Tumour su
C 684	16	3.2	2346	6	AKB87022	A. hydrop	Ahy87022	C 757	16	3.2	6626	4	AAS46809	Tumour su
C 685	16	3.2	2382	6	AAAS94828	Human DNA	HumDNA	C 758	16	3.2	7471	3	AAZ88789	B. subtil
C 686	16	3.2	2409	2	AAQ12084	C-termina	Cterm12084	C 759	16	3.2	7499	1	AAN91312	PCHL1 pla
C 687	16	3.2	2410	7	ABT41885	Toxicity	Tox41885	C 760	16	3.2	7502	2	AAQ27429	PCTD. 3/2
C 688	16	3.2	2410	9	ADB58172	Toxicity-	Tox58172	C 761	16	3.2	7603	6	ABL32308	Human imm
C 689	16	3.2	2410	9	ADB52670	Primary r	Prim52670	C 762	16	3.2	7603	6	ABL54329	Chemical
C 690	16	3.2	2469	4	ABL18522	Drosophil	Dros18522	C 763	16	3.2	8044	4	AAS46626	Tumour su
C 691	16	3.2	2481	5	AAS70479	DNA encod	DNA70479	C 764	16	3.2	8259	4	ABL16826	Drosophil
C 692	16	3.2	2481	5	AAS70479	DNA encod	DNA70479	C 765	16	3.2	8326	4	AAS90175	Human dig
C 693	16	3.2	2483	4	RAF87119	NOV8 codi	NOV87119	C 766	16	3.2	8326	5	AAK39819	Genomic s
C 694	16	3.2	2512	4	AAF87117	NOV6 codi	NOV67117	C 767	16	3.2	8326	8	ABD32779	Human nov
C 695	16	3.2	2546	2	AAAX13180	Enterococ	Ent13180	C 768	16	3.2	8444	6	ABT08487	Human nov
C 696	16	3.2	2546	6	ABS98975	Enterococ	Ent98975	C 769	16	3.2	8807	4	AAS35915	Human car
C 697	16	3.2	2580	6	ABZ13699	Arabidops	Arab13699	C 770	16	3.2	8807	9	AAD46609	Human car
C 698	16	3.2	2580	7	ADA67958	Arabidops	Arab67958	C 771	16	3.2	8990	4	AAK77783	Human imm
C 699	16	3.2	2581	4	ABL12794	Drosophil	Dros12794	C 772	16	3.2	9193	6	ABL46346	Human nuc
C 700	16	3.2	2631	9	ADC77525	Zebrafish	Zeb77525	C 773	16	3.2	9733	6	ABL32683	Human imm
C 701	16	3.2	2652	4	AAS06756	Polynucle	Pol06756	C 774	16	3.2	10311	4	AAK84424	Human imm
C 702	16	3.2	2686	4	AAS113465	DNA encod	DNA113465	C 775	16	3.2	10312	4	AAK84423	Human imm
C 703	16	3.2	2688	7	ACC78318	DNA encod	DNA78318	C 776	16	3.2	11009	6	ABQ72907	Mouse lam
C 704	16	3.2	2720	8	ABQ83445	Human ade	Humade83445	C 777	16	3.2	11009	6	AAI70816	Mouse lam
C 705	16	3.2	2806	8	ABZ57829	Mycobacte	Myco57829	C 778	16	3.2	11131	4	ABL09428	Drosophil
C 706	16	3.2	3003	4	AAH54803	S. epider	Sepe4803	C 779	16	3.2	11691	6	ABL34241	Human imm
C 707	16	3.2	3013	2	AAV01451	Plasmid p	Plas01451	C 780	16	3.2	11694	4	AAS46697	Tumour su
C 708	16	3.2	3150	2	AAV05542	Actinobac	Actin05542	C 781	16	3.2	12202	4	ABL21186	Drosophil
C 709	16	3.2	3172	4	ABL04524	Drosophil	Dros04524	C 782	16	3.2	12202	4	ABL202770	Drosophil
C 710	16	3.2	3215	4	AAAS04041	Human ABC	HumABC04041	C 783	16	3.2	12263	6	ABK84514	Human cdn
C 711	16	3.2	3254	7	ABQ83446	Human ade	Humade83446	C 784	16	3.2	12711	6	ABL34525	Human met
C 712	16	3.2	3260	6	ABT08489	Human nov	Humnov8489	C 785	16	3.2	12711	6	ABL70250	Chemical
C 713	16	3.2	3572	8	ACA98949	cDNA enco	cDNA98949	C 786	16	3.2	13732	6	ABL33820	Human imm
C 714	16	3.2	3623	4	AAI93584	Human pol	Humpol93584	C 787	16	3.2	15297	6	ABA94501	Human pro
C 715	16	3.2	3625	4	AAF87120	NOV9 codi	NOV97120	C 788	16	3.2	15297	7	ABV75414	Human kin
C 716	16	3.2	3660	9	ADB84153	Gene expr	Gene84153	C 789	16	3.2	17722	4	ABL03508	Drosophil
C 717	16	3.2	3723	7	ACA44526	Prokaryot	Prok44526	C 790	16	3.2	19211	3	AAA81507	N. mening
C 718	16	3.2	3908	4	AAZ25749	Tobacco i	Tobacco25749	C 791	16	3.2	20284	3	AAC69139	Human ABC
C 719	16	3.2	3957	9	ADD42744	Chlamydia	Chlam42744	C 792	16	3.2	21606	4	AAS62333	Human car
C 720	16	3.2	4027	4	ABL21187	Drosophil	Dros21187	C 793	16	3.2	21606	9	ADK46927	Human car
C 721	16	3.2	4111	5	ABA83184	HOST-5 (N	HOST583184	C 794	16	3.2	21732	4	AAK90176	Human dig
C 722	16	3.2	4135	4	AAF25742	Tobacco p	Tobacco25742	C 795	16	3.2	21732	5	AAS39820	Genomic s
C 723	16	3.2	4135	6	ABS76479	cDNA enco	cDNA76479	C 796	16	3.2	21732	8	ADK32780	Human nov
C 724	16	3.2	4137	3	AAZ20278	Borrelia	Bor20278	C 797	16	3.2	23272	7	ACC69138	Human tum
C 725	16	3.2	4137	3	AAA75484	DNA encod	DNA75484	C 798	16	3.2	27377	6	ABK89433	Human tum
C 726	16	3.2	4141	9	ADE57243	Rat gene	Rat57243	C 799	16	3.2	29596	4	ABL28638	Human che
C 727	16	3.2	4149	4	ABL02771	Drosophil	Dros02771	C 800	16	3.2	29993	9	ADB37660	Human che
C 728	16	3.2	4269	4	ABL17138	Drosophil	Dros17138	C 801	16	3.2	30143	4	ABL18664	Drosophil
C 729	16	3.2	4276	6	ABA04662	Human Hy	HumHy04662	C 802	16	3.2	33479	4	ABL19368	Drosophil
C 730	16	3.2	4580	4	ABL13746	Drosophil	Dros13746	C 803	16	3.2	34548	6	ABL70603	Chemical
C 731	16	3.2	4603	7	ABZ09973	Haematopo	Haemat09973	C 804	16	3.2	38342	4	AAS46745	Tumour su
C 732	16	3.2	4603	7	ABZ10119	Haematopo	Haemat10119	C 805	16	3.2	38342	6	ABK31506	Signal tr
C 733	16	3.2	4642	7	ABX13822	cDNA enco	cDNA13822	C 806	16	3.2	50000	6	AAD26437	Human GRM
C 734	16	3.2	4688	4	AAH17658	Human CDN	HumCDN17658	C 807	16	3.2	50000	6	AAD26400	Human glu
C 735	16	3.2	4799	4	ABL11598	Drosophil	Dros11598	C 808	16	3.2	66494	6	ABQ88140	Human ost
C 736	16	3.2	4835	3	AAZ79622	Virulence	Virul79622	C 809	16	3.2	70768	6	AAI41152	Wooden le
C 737	16	3.2	4835	6	ABQ83499	Pasteurel	Paste83499	C 810	16	3.2	77287	8	AAD58261	Murine tu
C 738	16	3.2	4962	7	ABX13823	cDNA enco	cDNA13823	C 811	16	3.2	102457	8	ACH03408	Murine tu
C 739	16	3.2	5171	2	AAV74575	Staphyloc	Staphy74575	C 812	16	3.2	110000	2	AAT58840	Continuation (3 of
C 740	16	3.2	5430	7	ACA19635	Prokaryot	Prok19635	C 813	16	3.2	110000	2	AAT58840	Continuation (3 of
C 741	16	3.2	5463	6	ABQ71011	Listeria	List71011	C 814	16	3.2	110000	2	AAV30458	Continuation (4 of
C 742	16	3.2	5636	4	AAS59561	Propionib	Prop59561	C 815	16	3.2	110000	2	AAV30458	Continuation (4 of
C 743	16	3.2	5636	7	ACF64490	Propionib	Prop64490	C 816	16	3.2	110000	2	AAV30459	Continuation (4 of
C 744	16	3.2	5794	6	ABS76450	cDNA enco	cDNA76450	C 817	16	3.2	110000	3	AAK20248	Continuation (10 of
C 745	16	3.2	5798	6	ABL32169	Human imm	Humimm32169	C 818	16	3.2	110000	3	AAK20248	Continuation (10 of
C 746	16	3.2	5798	6	ABQ67012	Human ang	Humang67012	C 819	16	3.2	110000	4	AAI99682	Continuation (19 of
C 747	16	3.2	6047	6	ABL65188	Lung canc	Lung65188	C 820	16	3.2	110000	6	AAI99683	Continuation (19 of
C 748	16	3.2	6047	6	ABK83721	Human cdn	Humcdn83721	C 821	16	3.2	110000	6	ABA92787	Continuation (2 of
C 749	16	3.2	6122	2	AAT87042	Branched	Branch87042	C 822	16	3.2	110000	6	ABA92787	Continuation (2 of
C 750	16	3.2	6122	4	AAF28392	Pseudomon	Pseudo28392	C 823	16	3.2	110000	6	ABQ59245	Continuation (12 of
C 751	16	3.2	6478	4	AAS45416	Chemical	Chem45416	C 824	16	3.2	110000	6	ABQ59245	Continuation (12 of
C 752	16	3.2	6478	6	ABK28269	DNA trans	DNA28269	C 825	16	3.2	110000	6	ABQ67197	Continuation (22 of
C 753	16	3.2	6478	6	ABN80200	Human che	Humche80200	C 826	16	3.2	110000	6	ABA03041	Continuation (11 of

827	16	3.2	110000	7	ACF67367_26	Continuation (27 o	C 900	15	3.0	327	2	AAV18560	Aav18560 Erwinia c
828	16	3.2	110000	7	ACF67367_27	Continuation (28 o	C 901	15	3.0	327	2	AAV18596	Aav18596 Erwinia c
829	16	3.2	110000	7	ACF67367_40	Continuation (41 o	C 902	15	3.0	327	2	AAV82359	Aav82359 DNA encod
830	16	3.2	110000	7	ACF65388_07	Continuation (8 of	C 903	15	3.0	327	9	AH222082	Aah222082 Erwinia c
831	16	3.2	110000	7	ACF65388_1	Continuation (2 of	C 904	15	3.0	327	9	AD65043	Adc65043 Immunoglo
832	16	3.2	110000	7	ACF53224_2	Continuation (3 of	C 905	15	3.0	328	3	AA13121	Aac13121 Human sec
833	16	3.2	110608	6	ABK83572_1	Continuation (3 of	C 906	15	3.0	329	4	AH69435	Aah69435 Human cer
834	16	3.2	146547	7	ABZ80817	Abz80817 Human pho	C 907	15	3.0	333	6	ABN22147	Abn22147 Human ORF
835	16	3.2	167739	8	AD58258	Ad58258 Murine tu	C 908	15	3.0	333	7	ACA40978	Ac40978 Prokaryot
836	16	3.2	183999	4	AAFP2881	Aaf2881 Human ABC	C 909	15	3.0	334	6	ABZ35596	Abz35596 Human Gen
837	16	3.2	213251	6	ABQ67193	Abq67193 Listeria	C 910	15	3.0	336	7	ABX48756	Abx48756 Bovine ES
838	16	3.2	265118	5	AAH41227	Aah41227 Pyrococcu	C 911	15	3.0	336	7	ACA41320	Ac41320 Prokaryot
839	16	3.2	349380	5	AAH41227	Aah41227 Pyrococcu	C 912	15	3.0	336	7	ACA48620	Ac48620 Prokaryot
840	16	3.2	349380	3	AAH21609	Aaf21609 Neisseria	C 913	15	3.0	338	7	ABZ72375	Abz72375 Rice leaf
841	15	3.0	51	4	AA131171	Aal131171 Human SNP	C 914	15	3.0	341	6	ABK78233	Abk78233 Bacillus
842	15	3.0	59	3	AAAL3818	Aaal3818 Diptheri	C 915	15	3.0	344	5	AAF67129	Aaf67129 Novel hum
843	15	3.0	59	7	ADA88975	Ada88975 S. coelic	C 916	15	3.0	347	3	AAC28523	Aac28523 Human sec
844	15	3.0	59	7	ADA88969	Ada88969 S. coelic	C 917	15	3.0	349	4	AAI84920	Aai84920 Human pol
845	15	3.0	59	7	ADA88977	Ada88977 S. coelic	C 918	15	3.0	351	7	ACA46803	Ac46803 Prokaryot
846	15	3.0	59	7	ADA88977	Ada88977 S. coelic	C 919	15	3.0	351	8	ADB12007	Adb12007 Alloococ
847	15	3.0	74	2	AA150128	Aai50128 Human foe	C 920	15	3.0	352	4	AAI16460	Aai16460 Probe #63
848	15	3.0	90	7	ABZ79185	Abz79185 Tumour su	C 921	15	3.0	352	4	AB559414	Ab559414 Human foe
849	15	3.0	90	7	ABZ09732	Abz09732 Human oli	C 922	15	3.0	352	4	AAI39230	Aai39230 Probe #79
850	15	3.0	100	7	ACD74569	Ac74569 E. coli K	C 923	15	3.0	352	4	ABA28085	Ab28085 Probe #65
851	15	3.0	117	2	AAQ02896	Aaq02896 Gene enco	C 924	15	3.0	352	4	AAK33454	Aak33454 Human bon
852	15	3.0	136	4	ABA70015	Ab70015 Human foe	C 925	15	3.0	352	4	AAK07646	Aak07646 Human bra
853	15	3.0	136	4	AAI50128	Aai50128 Human gen	C 926	15	3.0	352	4	ABS33212	Abs33212 Human liv
854	15	3.0	136	4	AAK44120	Aak44120 Human bon	C 927	15	3.0	352	6	ABS08298	Ab508298 Human gen
855	15	3.0	136	4	AAK18224	Aak18224 Human bra	C 928	15	3.0	354	3	AA50093	Aas50093 Arabidops
856	15	3.0	136	4	ABS43776	Abs43776 Human liv	C 929	15	3.0	354	7	ABZ38568	Abz38568 N. gonorr
857	15	3.0	136	6	ABS18355	Abs18355 Human gen	C 930	15	3.0	364	4	AAI11550	Aai11550 Human bre
858	15	3.0	138	3	AA132571	Aac32571 Human sec	C 931	15	3.0	390	8	ACH29214	Ach29214 Human adu
859	15	3.0	146	2	AAV7001	Aav7001 Staphyloc	C 932	15	3.0	391	4	AAI81341	Aai81341 Human pol
860	15	3.0	149	6	ABL93149	Ab193149 Rat metas	C 933	15	3.0	393	2	AAV85536	Aav85536 EST clone
861	15	3.0	155	4	AA548653	Aas48653 Pseudomon	C 934	15	3.0	393	9	ADC90897	Adc90897 E. faeciu
862	15	3.0	155	4	AA548677	Aas48677 Pseudomon	C 935	15	3.0	396	4	AA560349	Aas60349 Human can
863	15	3.0	155	7	ACAI5717	Ac5717 Prokaryot	C 936	15	3.0	398	5	ABV16707	Abv16707 Human pro
864	15	3.0	155	7	ACAI5695	Ac5695 Prokaryot	C 937	15	3.0	399	8	ACH19365	Ach19365 Human adu
865	15	3.0	165	7	ACF68492	Acf68492 Phototrab	C 938	15	3.0	401	7	ABX41628	Abx41628 Bovine ES
866	15	3.0	232	3	AA161170	Aac16170 Human sec	C 939	15	3.0	401	8	ACH16527	Ach16527 Human adu
867	15	3.0	237	7	ABX49911	Abx49911 Bovine ES	C 940	15	3.0	402	4	AAI20448	Aai20448 Human bre
868	15	3.0	256	3	AAH11164	Aaah1164 Partial h	C 941	15	3.0	402	5	AA575093	Aas75093 DNA encod
869	15	3.0	268	3	ABN81035	Abn81035 Shrimp po	C 942	15	3.0	403	4	AAI16177	Aai16177 Human bre
870	15	3.0	269	2	AAH20837	Aat20837 Human gen	C 943	15	3.0	403	7	ABX38783	Abx38783 Bovine ES
871	15	3.0	271	6	ABN79571	Abn79571 Human ORF	C 944	15	3.0	405	4	AA560725	Aas60725 Human can
872	15	3.0	288	6	ABU71824	Ab171824 Corn tass	C 945	15	3.0	405	7	ABZ38569	Abz38569 N. gonorr
873	15	3.0	290	3	AAU05902	Aac05902 Human sec	C 946	15	3.0	408	6	ABN19454	Abn19454 Human ORF
874	15	3.0	300	2	AAZ14921	Aaz14921 Human gen	C 947	15	3.0	410	4	AAI14598	Aai14598 Human bre
875	15	3.0	300	2	AAZ14965	Aaz14965 Human gen	C 948	15	3.0	412	7	ABX41629	Abx41629 Bovine ES
876	15	3.0	301	3	AAO6464	Aao6464 Human imm	C 949	15	3.0	413	7	ABX48625	Abx48625 Bovine ES
877	15	3.0	301	4	AAH93580	Aah93580 Human pro	C 950	15	3.0	416	6	ABK45258	Abk45258 cDNA enco
878	15	3.0	301	4	AA563672	Aas63672 Human pro	C 951	15	3.0	420	4	AA537340	Aas37340 Novel hum
879	15	3.0	301	4	AAH02645	Aah02645 Prostate	C 952	15	3.0	428	6	ABL65118	Ab165118 Lung canc
880	15	3.0	301	4	AAH84894	Aah84894 Human pro	C 953	15	3.0	428	6	ABL64604	Ab164604 Stomach c
881	15	3.0	301	4	AAH10934	Aah10934 Human CDN	C 954	15	3.0	428	6	ABN95527	Abn95527 Gene #202
882	15	3.0	301	5	ACAS9481	Acas9481 Prostate	C 955	15	3.0	429	4	AAU00909	Aal00909 Human rep
883	15	3.0	301	6	ABL95044	Ab195044 Human JPT	C 956	15	3.0	433	7	ACA14047	Ac414047 Prokaryot
884	15	3.0	301	7	ACC95208	Acc95208 Prostate	C 957	15	3.0	437	6	ABQ99210	Abq99210 Human ORF
885	15	3.0	301	9	ADB13681	Adb13681 Human pro	C 958	15	3.0	439	4	AB530426	Abs30426 DNA encod
886	15	3.0	303	4	AAH72913	Aah72913 Human cer	C 959	15	3.0	439	4	AAU04459	Aal04459 Human rep
887	15	3.0	303	4	AAH72313	Aah72313 Human cer	C 960	15	3.0	440	3	AAU01475	Aac01475 Human sec
888	15	3.0	307	6	AAH70770	Aah70770 Human cer	C 961	15	3.0	444	7	ABX06836	Abx06836 S. pneumo
889	15	3.0	307	6	ABL80727	Ab180727 Human ova	C 962	15	3.0	444	7	ABX06836	Abx06836 S. pneumo
890	15	3.0	309	3	AAU09054	Aac09054 Human sec	C 963	15	3.0	444	7	ACA27802	Ac27802 Prokaryot
891	15	3.0	312	9	ADB51263	Adb51263 Primary r	C 964	15	3.0	447	4	AAI86120	Aai86120 Human pol
892	15	3.0	319	5	ABAI6888	Abai6888 Human ner	C 965	15	3.0	451	6	ABK39609	Abk39609 cDNA enco
893	15	3.0	319	5	ABAI6889	Abai6889 Human ner	C 966	15	3.0	451	7	ACA11938	Aac11938 Human lun
894	15	3.0	319	5	ABAI6890	Abai6890 Human ner	C 967	15	3.0	451	7	ACA03124	Aca03124 Lung canc
895	15	3.0	320	2	AAK33648	Aak33648 DNA tande	C 968	15	3.0	453	6	ABN70560	Abn70560 Streptoco
896	15	3.0	327	1	AAU90302	Aan90302 Pectate l	C 969	15	3.0	453	6	ABV95846	Abv95846 Human pan
897	15	3.0	327	1	AAU51044	Aat51044 Pel B sig	C 970	15	3.0	453	6	ABV95579	Abv95579 Human pan
898	15	3.0	327	2	AAU70874	Aat70874 Erwinia c	C 971	15	3.0	455	4	AA524617	Aas24617 Human ova
899	15	3.0	327	2	AAU03933	Aav03933 Erwinia c	C 972	15	3.0	455	5	AAH83240	Aah83240 Human ova

973 15 3.0 456 7 ABZ40094
 c 974 15 3.0 457 5 ABV46505
 c 975 15 3.0 458 8 ACH18286
 c 976 15 3.0 460 4 AAS60350
 c 977 15 3.0 462 3 ARA69611
 c 978 15 3.0 462 4 AAS57753
 c 979 15 3.0 462 8 ACH18278
 c 980 15 3.0 463 4 ABA57389
 981 15 3.0 463 4 AAI36934
 982 15 3.0 463 4 AAK31024
 983 15 3.0 463 4 AAK05425
 984 15 3.0 463 4 ABS30703
 985 15 3.0 463 6 ABS05774
 c 986 15 3.0 468 8 ACH45182
 987 15 3.0 468 4 AAI92974
 988 15 3.0 468 5 ABV12629
 989 15 3.0 469 4 ABA57383
 990 15 3.0 469 4 AAI36927
 991 15 3.0 469 4 AAK31017
 992 15 3.0 469 4 AAK05418
 993 15 3.0 469 4 ABS30696
 994 15 3.0 469 6 ABS05767
 995 15 3.0 470 4 AAI13970
 996 15 3.0 470 4 ABA55698
 997 15 3.0 470 4 AAI35353
 998 15 3.0 470 4 ABA45208
 999 15 3.0 470 4 ABA25385
 1000 15 3.0 470 4 AAK29393

ALIGNMENTS

RESULT 1
 ABQ73179
 ID ABQ73179 standard; DNA; 500 BP.
 XX
 AC ABQ73179;
 XX

27-SEP-2002 (first entry)
 XX

C. glutamicum transcriptional regulatory region 1dh DNA SEQ ID NO:7.
 XX

Corynebacterium glutamicum; transcriptional regulation; gene expression;
 amino acid biosynthesis; gene; ds.
 XX

Corynebacterium glutamicum.
 OS

WO200240679-A2.
 XX

23-MAY-2002.
 XX

15-NOV-2001; 2001WO-US043096.
 XX

15-NOV-2000; 2000US-0248219P.
 XX

(RAYA/) RAYAPATI P J.
 XX

(CRAF/) CRAFTON C M.
 XX

Rayapati PJ, Crafton CM;
 PI

WPI; 2002-575217/61.
 XX

Novel polynucleotides from Corynebacterium glutamicum useful for inducing
 and regulating expression of genes, including those that are involved in
 amino acid biosynthesis, in bacterial cells.
 XX

Claim 20; Page 25; 112pp; English.
 PS

The present invention describes Corynebacterium glutamicum
 CC

transcriptional regulatory region polynucleotide sequences (I). ABQ73173
 CC

to ABQ73194 represent the C. glutamicum transcriptional regulatory
 CC

regions pra, aceA, aceB, adh, aldB, poxB, ldh, amyE, malZ, bglX, gam,
 CC

CC glgX, hisD, pyrR, purD, hrcA, htpX, dnaK, etc, grpB, clpB, and narX,
 CC respectively. (I) can be used for producing a vector. (I) can also be
 CC used for producing a transformed Corynebacterium sp. host cell, which is
 CC useful for producing a biosynthetic product. (I) is useful for producing
 CC a Corynebacterium sp. host cell, which is useful for producing an amino
 CC acid. (I) is useful for regulating and enhancing the production of a
 CC variety of products in host cells, including amino acids such as lysine,
 CC purine nucleotides such as inosinic acid, and heterologous polypeptides
 XX

Seq Sequence 500 BP; 127 A; 110 C; 145 G; 118 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 6; Length 500;

Best Local Similarity 100.0%; Pred. No. 7.3e-248;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACCACCGGTTTCGGCAACAATGACGGCAGAGA 60

Db 1 AAAACAGCCAGGTTAGCGGCTGTAAACCCACCACCGGTTTCGGCAACAATGACGGCAGAGA 60

QY 61 GCCCACCACATTTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTTCAGGGAGGATT 120

Db 61 GCCCACCACATTTGCGATTTCGCTCCGATAAAGCCAGCGCCCATATTTTCAGGGAGGATT 120

QY 121 CGCCTGCGGTTTGGCGACATTCGGATCCCGGACCGAGCTCTGCAATGACCTGCGCGCG 180

Db 121 CGCCTGCGGTTTGGCGACATTCGGATCCCGGACCGAGCTCTGCAATGACCTGCGCGCG 180

QY 181 AGGGAAGCGAGGTGGGTGGCGAGTTTGTAGTCCGGGTTTAAAGCTTGCAGGCGAGTGCTG 240

Db 181 AGGGAAGCGAGGTGGGTGGCGAGTTTGTAGTCCGGGTTTAAAGCTTGCAGGCGAGTGCTG 240

QY 241 AGCAAAAGCGCTAGTCTCTGGGAGCGAAACCATATTTAGATCATCTTGGCAGAGCATGCA 300

Db 241 AGCAAAAGCGCTAGTCTCTGGGAGCGAAACCATATTTAGATCATCTTGGCAGAGCATGCA 300

QY 301 ATTTCTGAGGCGATAGATTGGTTTGTCTCGATTTTACATGATGATTTTTCACAAAAATA 360

Db 301 ATTTCTGAGGCGATAGATTGGTTTGTCTCGATTTTACATGATGATTTTTCACAAAAATA 360

QY 361 ACATCTGCTGTACACCATTTTCGGACATATTCGGGATATTAAGGTGTAAACAAGGA 420

Db 361 ACATCTGCTGTACACCATTTTCGGACATATTCGGGATATTAAGGTGTAAACAAGGA 420

QY 421 ATCCGGGCACAAAGCTCTTGTGATTTTCTGAGCTGCTTTGGGTTGTCCGGTTAGGAA 480

Db 421 ATCCGGGCACAAAGCTCTTGTGATTTTCTGAGCTGCTTTGGGTTGTCCGGTTAGGAA 480

QY 481 ATCAGGAAGTGGGATCGAAA 500

Db 481 ATCAGGAAGTGGGATCGAAA 500

RESULT 2

AAH68534/C

ID AAH68534 standard; DNA; 309400 BP.

XX

AC AAH68534;

XX

DT 26-SEP-2001 (first entry)

XX

C glutamicum coding sequence fragment SEQ ID NO: 7069.

DE

Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KW

organic acid synthesis; ds.

XX

Corynebacterium glutamicum.

OS

EP1108790-A2.

XX

20-JUN-2001.

PD

18-DEC-2000; 2000EP-00127688.

PF

DT 03-JUN-2003 (first entry)
 XX C. glutamicum derived ORF SEQ ID 1181.
 XX
 KW Coryneform; nucleic acid array; fermentation; culture; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN DE10128510-A1.
 XX
 PD 19-DEC-2002.
 XX
 PF 13-JUN-2001; 2001DE-01028510.
 XX
 PR 13-JUN-2001; 2001DE-01028510.
 XX
 PA (DEGS) DEGUSSA AG.
 XX
 PI Farwick M, Moeckel B, Pfefferle W, Bathe B, Huthmacher K;
 XX WPI; 2003-279970/28.
 DR
 DR
 XX
 XX New nucleic acid array useful for monitoring mRNA expression of
 PT Corynebacterium glutamicum during fermentation, comprising nucleic acid
 PT from Corynebacterium glutamicum.
 XX
 XX Claim 1; Page 426-427; 709pp; German.
 PS
 PS
 CC This invention describes a novel nucleic acid array involving
 CC Corynebacterium glutamicum polynucleotides. The arrays are used to
 CC analyse C. glutamicum, particularly for monitoring a fermentation process
 CC to determine expression levels of C. glutamicum cellular mRNA. Such
 CC monitoring particularly differentiates between expression levels of
 CC different strains of C. glutamicum and allows the adjustment of different
 CC culture and fermentation conditions. ACA00010-ACA02188 represent C.
 CC glutamicum derived polynucleotides described in the disclosure of the
 CC invention
 CC
 XX SQ Sequence 1776 BP; 365 A; 505 C; 511 G; 395 T; 0 U; 0 Other;
 Query Match 26.8%; Score 134; DB 7; Length 1776;
 Best Local Similarity 100.0%; Pred. No. 8.7e-59;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 GTAACCCACACCGTTTCGGCAACAATGACGGCGAGAGAGCCACCACTTGGGATTTC 81
 Db 251 GTAACCCACACCGTTTCGGCAACAATGACGGCGAGAGAGCCACCACTTGGGATTTC 192
 QY 82 GCTCCGATAAGCCAGCGCCCATATTTGACGGAGGATTGCGCTGCGGTTTGGGACATT 141
 Db 191 GCTCCGATAAGCCAGCGCCCATATTTGACGGAGGATTGCGCTGCGGTTTGGGACATT 132
 QY 142 CGGATCCCGGAAC 155
 Db 131 CGGATCCCGGAAC 118
 RESULT 5
 ADD13410
 ID ADD13410 standard; DNA; 1084 BP.
 XX
 AC ADD13410;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 XX C. glutamicum carbon metabolism associated DNA RXA02694.
 DE
 DE ds; gene; carbon metabolism; energy-rich molecule;
 KW oxidative phosphorylation; fine chemical; amino acid production;
 KW lysine production; nucleotide production; nucleoside production;
 KW lipid production; fatty acid production; diol production;
 KW carbohydrate production; aromatic compound production;
 KW vitamin production; co-factor production; enzyme production; food;
 XX

KW animal feed; cosmetic; pharmaceutical.
 XX
 OS Corynebacterium glutamicum.
 XX
 FH Key Location/Qualifiers
 FT CDS 101..1057
 FT /*tag= a
 XX
 PN W02003040291-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 31-OCT-2002; 2002W0-EF012135.
 XX
 PR 05-NOV-2001; 2001DE-01054270.
 XX
 PA (BADI) BASF AG.
 XX
 PI Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;
 PI Haberhauser G;
 XX
 DR WPI; 2003-505068/47.
 DR P-PSDB; ADD13411.
 XX
 XX New nucleic acid encoding variant forms of proteins involved in carbon
 PT compound metabolism, useful for production of fine chemicals,
 PT specifically lysine, in microorganisms.
 PT
 XX
 XX Claim 1; SEQ ID NO 95; 259pp; German.
 PS
 PS This invention describes novel polynucleotides and polypeptides
 CC associated with the metabolism of carbon compounds and generation of
 CC energy-rich molecules by oxidative phosphorylation in Corynebacterium
 CC glutamicum. The polynucleotides of the invention are isolated from a
 CC nucleic acid library of C. glutamicum then mutated at the specified
 CC positions, cloned and expressed by standard methods. Cells, especially
 CC Corynebacterium glutamicum, containing vectors that express the
 CC polynucleotides are used for production of fine chemicals, preferably
 CC amino acids and specifically lysine, but more generally nucleotides,
 CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, co-factors and enzymes. These are useful in the
 CC food, animal feed, cosmetics and pharmaceutical industries.
 CC Polynucleotides, optionally as primers and probes, can also be used for
 CC identification and classification of C. glutamicum and related species,
 CC e.g. for diagnosis; for genomic mapping; functional or evolutionary
 CC studies gene manipulation, and modulation of metabolic activity. Cells
 CC that contain the products of the invention may produce fine chemicals in
 CC better yields, with higher productivity and/or more efficiently.
 XX
 XX SQ Sequence 1084 BP; 270 A; 308 C; 285 G; 221 T; 0 U; 0 Other;
 Query Match 22.4%; Score 112; DB 9; Length 1084;
 Best Local Similarity 100.0%; Pred. No. 2e-47;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 389 TAATCGGGCATAATTAAAGGTGTAAACAAGGAATCCGGGCACAAAGCTCTTGTGATTTC 448
 Db 1 TAATCGGGCATAATTAAAGGTGTAAACAAGGAATCCGGGCACAAAGCTCTTGTGATTTC 60
 QY 449 TGAGCTGCTTTTGGGTTGTCCGGTTAGGGAATCAGGAATCGGATCGAA 500
 Db 61 TGAGCTGCTTTTGGGTTGTCCGGTTAGGGAATCAGGAATCGGATCGAA 112
 RESULT 6
 AAF71424
 ID AAF71424 standard; DNA; 1065 BP.
 XX
 AC AAF71424;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:129.

XX Corynebacterium glutamicum; carbon metabolism and energy production;
 KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
 KW fine chemical production; organic acid; proteinogenic amino acid;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
 KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
 KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
 KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
 XX
 OS Corynebacterium glutamicum.

XX WO200100844-A2.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB000943.

XX 25-JUN-1999; 99US-0141031P.

XX 08-JUL-1999; 99DE-01031412.

XX 08-JUL-1999; 99DE-01031413.

XX 08-JUL-1999; 99DE-01031419.

XX 08-JUL-1999; 99DE-01031420.

XX 08-JUL-1999; 99DE-01031424.

XX 08-JUL-1999; 99DE-01031428.

XX 08-JUL-1999; 99DE-01031431.

XX 08-JUL-1999; 99DE-01031433.

XX 08-JUL-1999; 99DE-01031434.

XX 08-JUL-1999; 99DE-01031510.

XX 08-JUL-1999; 99DE-01031562.

XX 08-JUL-1999; 99DE-01031634.

XX 09-JUL-1999; 99DE-01032180.

XX 09-JUL-1999; 99DE-01032227.

XX 09-JUL-1999; 99DE-01032230.

XX 09-JUL-1999; 99US-0143208P.

XX 14-JUL-1999; 99DE-01032924.

XX 14-JUL-1999; 99DE-01032973.

XX 14-JUL-1999; 99DE-01033005.

XX 27-AUG-1999; 99DE-01040765.

XX 31-AUG-1999; 99US-0151572P.

XX 03-SEP-1999; 99DE-01042076.

XX 03-SEP-1999; 99DE-01042079.

XX 03-SEP-1999; 99DE-01042086.

XX 03-SEP-1999; 99DE-01042087.

XX 03-SEP-1999; 99DE-01042088.

XX 03-SEP-1999; 99DE-01042095.

XX 03-SEP-1999; 99DE-01042123.

XX 03-SEP-1999; 99DE-01042125.

XX (BADI) BASF AG.

XX Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

XX P-PSDB; AAB79307.

XX WPI: 2001-061975/07.
 XX P-PSDB; AAB79307.
 XX
 XX New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
 XX metabolism and oxidative phosphorylation protein for production or
 XX modulation of production of fine chemicals e.g. amino acids,
 XX carbohydrates or enzymes.

XX Claim 3; Page 332-333; 1246pp; English.

XX AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
 XX metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
 XX to AAB 79633 which are involved in carbon metabolism and energy
 XX production. The C. glutamicum SMP gene can be used in vectors (ii) for
 XX expression in host cells and production or modulation of production of
 XX fine chemicals, such as, an organic acid, a proteinogenic or
 XX nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
 XX nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
 XX a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
 XX polyketide, or an enzyme. The presence of (i) or SMP proteins (iii)
 XX encoded by them are used for diagnosing the presence or activity of

CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
 CC containing them are used to map genomes of organisms related to C.
 CC glutamicum, identify and localise C. glutamicum sequences of interest, in
 CC evolutionary studies, in determining SMP protein regions required for
 CC function, in modulating SMP protein activity, in modulating the
 CC metabolism of sugars, and in modulating high-energy molecule production
 CC in a cell (i.e. ATP, NADPH)
 XX
 SQ Sequence 1065 BP; 264 A; 304 C; 279 G; 218 T; 0 U; 0 Other;

Query Match 20.0%; Score 100; DB 4; Length 1065;
 Best Local Similarity 100.0%; Pred. No. 3.2e-41;
 Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 401 ATTAAAGGTGTAAACAAAGGAATCCGGGCACAAAGCTCTTCTGATTTCTGAGCTGCTTTG 460
 Db |||||
 QY 461 TGGGTTGTCGGTTAGGGAATCAGGAATCGGATCGGAA 500
 Db |||||
 61 TGGGTTGTCGGTTAGGGAATCAGGAATCGGATCGGAA 100

RESULT 7

AAC48302

ID AAC48302 standard; DNA; 579 BP.

XX AAC48302;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 56987.

XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

XX 23-APR-1999; 99US-0130510P.

XX 23-APR-1999; 99US-0130891P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 04-MAY-1999; 99US-0132407P.

XX 30-APR-1999; 99US-0132484P.

XX 05-MAY-1999; 99US-0132485P.
 XX 06-MAY-1999; 99US-0132486P.
 XX 07-MAY-1999; 99US-0132487P.
 XX 11-MAY-1999; 99US-0132863P.
 XX 14-MAY-1999; 99US-0134256P.
 XX 14-MAY-1999; 99US-0134219P.
 XX 14-MAY-1999; 99US-0134221P.
 XX 14-MAY-1999; 99US-0134370P.
 XX 18-MAY-1999; 99US-0134768P.

PR	28-JUL-1999;	99US-0145951P;
PR	02-AUG-1999;	99US-0146388P;
PR	02-AUG-1999;	99US-0146388P;
PR	02-AUG-1999;	99US-0146389P;
PR	03-AUG-1999;	99US-0147038P;
PR	04-AUG-1999;	99US-0147204P;
PR	04-AUG-1999;	99US-0147302P;
PR	05-AUG-1999;	99US-0147192P;
PR	06-AUG-1999;	99US-0147260P;
PR	06-AUG-1999;	99US-0147303P;
PR	06-AUG-1999;	99US-0147416P;
PR	09-AUG-1999;	99US-0147493P;
PR	09-AUG-1999;	99US-0147935P;
PR	10-AUG-1999;	99US-0148171P;
PR	11-AUG-1999;	99US-0148319P;
PR	12-AUG-1999;	99US-0148341P;
PR	13-AUG-1999;	99US-0148565P;
PR	13-AUG-1999;	99US-0148684P;
PR	16-AUG-1999;	99US-0149368P;
PR	17-AUG-1999;	99US-0149175P;
PR	18-AUG-1999;	99US-0149426P;
PR	20-AUG-1999;	99US-0149722P;
PR	20-AUG-1999;	99US-0149723P;
PR	20-AUG-1999;	99US-0149902P;
PR	23-AUG-1999;	99US-0149902P;
PR	23-AUG-1999;	99US-0149930P;
PR	25-AUG-1999;	99US-0150566P;
PR	26-AUG-1999;	99US-0150884P;
PR	27-AUG-1999;	99US-0151065P;
PR	27-AUG-1999;	99US-0151066P;
PR	27-AUG-1999;	99US-0151080P;
PR	27-AUG-1999;	99US-0151303P;
PR	31-AUG-1999;	99US-0151438P;
PR	01-SEP-1999;	99US-0151930P;
PR	07-SEP-1999;	99US-0152363P;
PR	10-SEP-1999;	99US-0153700P;
PR	13-SEP-1999;	99US-0153758P;
PR	15-SEP-1999;	99US-0154018P;
PR	16-SEP-1999;	99US-0154039P;
PR	20-SEP-1999;	99US-0154779P;
PR	22-SEP-1999;	99US-0155139P;
PR	23-SEP-1999;	99US-0155486P;
PR	24-SEP-1999;	99US-0155653P;
PR	28-SEP-1999;	99US-0156458P;
PR	29-SEP-1999;	99US-0156596P;
PR	04-OCT-1999;	99US-0157117P;
PR	05-OCT-1999;	99US-0157753P;
PR	06-OCT-1999;	99US-0157865P;
PR	07-OCT-1999;	99US-0158023P;
PR	08-OCT-1999;	99US-0158232P;
PR	12-OCT-1999;	99US-0158369P;
PR	14-OCT-1999;	99US-0159320P;
PR	14-OCT-1999;	99US-0159331P;
PR	14-OCT-1999;	99US-0159637P;
PR	14-OCT-1999;	99US-0159638P;
PR	18-OCT-1999;	99US-0159294P;
PR	13-OCT-1999;	99US-0159293P;
PR	13-OCT-1999;	99US-0159294P;
PR	21-OCT-1999;	99US-0160815P;
PR	22-OCT-1999;	99US-0160980P;
PR	22-OCT-1999;	99US-0160981P;
PR	21-OCT-1999;	99US-0160767P;
PR	21-OCT-1999;	99US-0160768P;
PR	21-OCT-1999;	99US-0160770P;
PR	21-OCT-1999;	99US-0160814P;
PR	21-OCT-1999;	99US-0160815P;
PR	25-OCT-1999;	99US-0161405P;
PR	25-OCT-1999;	99US-0161406P;
PR	26-OCT-1999;	99US-0161359P;

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PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 26-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 4.6%; Score 23; DB 3; Length 579;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 437 TTGCTGATTTCTGAGCTGCTTT 459
Db 82 TTGCTGATTTCTGAGCTGCTTT 104

RESULT 8
AAC34575
ID AAC34575 standard; DNA; 580 BP.
XX
AC AAC34575;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7133.
XX
KW Hybridisation assay; Genetic mapping; Gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
FF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
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PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131445P.
PR 30-APR-1999; 99US-0132048P.
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PR 06-MAY-1999; 99US-0132486P.
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PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
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PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139763P.
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PR 01-JUL-1999; 99US-0141842P.
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PR 19-JUL-1999; 99US-0144332P.
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PR 19-JUL-1999; 99US-0144334P.
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PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
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Query Match 3.8%; Score 19; DB 8; Length 497;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 475 AGGGAATCAGGAAGTGGG 493
 Db |||||
 96 AGGGAATCAGGAAGTGGG 78

RESULT 10

ABT42792/c
 ID ABT42792 standard; DNA; 852 BP.

XX AC ABT42792;
 XX AC

DT 22-SEP-2003 (first entry)

XX Human neuroblastoma-related DNA sequence, SEQ ID NO:73.

DE Human; ds; neuroblastoma; prognosis.

XX Homo sapiens.

XX WO2002103017-A1.

PN PD 27-DEC-2002.

PF 30-MAY-2002; 2002WO-JP005295.

PR 31-MAY-2001; 2001JP-00163666.

PR 24-AUG-2001; 2001JP-00255260.

PA (CHTB-) CHIBA PREFECTURE.

XX (HISM) HISAMITSU PHARM CO LTD.

PI Nakagawara A;

DR WPI; 2003-167523/16.

PT Nucleic acids isolated from neuroblastoma showing enhanced expression in

PT human neuroblastoma with good prognosis, useful in clarifying good/poor

PT prognosis of neuroblastoma and providing genetic data.

XX Claim 1; Page 115-116; 444pp; Japanese.

XX The invention comprises DNA sequences that show enhanced expression in

XX human neuroblastoma with good prognosis. The DNA sequences of the

XX invention are useful in clarifying good/poor prognosis of neuroblastoma.

XX The present sequence represents a human neuroblastoma-related DNA

XX sequence of the invention

XX SQ Sequence 852 BP; 173 A; 152 C; 190 G; 198 T; 0 U; 139 Other;

Query Match 3.8%; Score 19; DB 7; Length 852;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 402 TTAAAGGTGTAACAAGGA 420
 Db |||||

535 TTAAAGGTGTAACAAGGA 517

RESULT 11
 ABN80060/c

ID ABN80060 standard; DNA; 6971 BP.

XX AC ABN80060;

XX 15-JUL-2002 (first entry)

XX Human chemically modified disease associated gene SEQ ID NO 77.

XX Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;

XX heart disease; epilepsy; histone deacetylation; muscular dystrophy;

XX dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;

XX antidiabetic; cytosine; anticonvulsant; ds.

OS Homo sapiens.
 OS Synthetic.

PN WO200200927-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP007536.

PF 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130908/17.

XX Novel nucleic acid useful for diagnosis and therapy of diseases

PT associated with development genes such as diabetes, comprises a sequence

PT of a segment of chemically pretreated DNA of genes associated with

PT development.

XX Claim 1; SEQ ID NO 77; 27pp; English.

XX The invention relates to a nucleic acid (I) comprising a sequence at

XX least 18 bases in length of a segment of chemically pretreated DNA (II)

XX of genes associated with development selected from 87 genes listed in the

XX specification such as ACCPN, ADFN, or AFDI and comprising one of 350

XX sequences (ABN79984-ABN80333) or their complements. The invention is

XX useful for the diagnosis or therapy of diseases associated with

XX development genes, in particular disease related to homeobox containing

XX genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes

XX associated with congenital heart disease, epilepsy, diseases related to

XX histone deacetylation, Currarino syndrome, diseases related with the

XX development of the brain and limb girdle muscular dystrophy and dwarfism.

XX Oligomers specific to each of the genes are useful for detecting the

XX methylation state of all CpG dinucleotides within the 350 sequences or

XX (II) and their complementary sequences, as primer oligonucleotides for

XX the amplification of the 350 sequences, (II) and/or their complements and

XX as oligomer probes for detecting the cytosine methylation state and/or

XX single nucleotide polymorphisms (SNPs). Note: The sequence data for this

XX patent did not form part of the printed specification but is based on

XX sequence information supplied to Derwent by the European Patent Office

XX SQ Sequence 6971 BP; 1776 A; 282 C; 1775 G; 3137 T; 0 U; 1 Other;

Query Match 3.8%; Score 19; DB 6; Length 6971;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 344 TTTTTCACACAAAATAAC 362
 Db |||||

421 TTTTTCACACAAAATAAC 403

RESULT 12
 ABL32467/c

ID ABL32467 standard; DNA; 15373 BP.

XX AC ABL32467;

XX 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 440.

XX Human; immune system disease; cytosine methylation; antiasthmatic;

XX antiarteriosclerotic; antianaemic; cytostatic; neutropic;

XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

XX antirheumatic; antarthritic; antidiabetic; antipsoriatic;

XX antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;

XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;

KW ds.
XX Homo sapiens.
OS WO200200928-A2.
XX
FN 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP007537.
XX
XX 30-JUN-2000; 2000DE-01032529.
XX
XX 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin X;
PI
XX WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
XX Claim 1; SEQ ID NO 440; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
XX Sequence 15373 BP; 5097 A; 89 C; 2465 G; 7722 T; 0 U; 0 Other;
SQ

Query Match 3.8%; Score 19; DB 6; Length 15373;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAATAAAC 362
Db 2883 TTTTTCACAAATAAAC 2865

RESULT 13
AAK58736
ID AAK58736 standard; cDNA; 109 BP.
XX
XX AAK58736;
AC
XX
XX 06-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3796.
DE
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ss.
KW
XX
XX Homo sapiens.
OS
XX WO200157182-A2.
FN
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
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XX 31-JAN-2000; 2000US-0179065P.
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XX 04-FEB-2000; 2000US-0180628P.
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XX 24-FEB-2000; 2000US-0184664P.
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XX 02-MAR-2000; 2000US-0186350P.
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XX 16-MAR-2000; 2000US-0189874P.
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XX 18-APR-2000; 2000US-0198123P.
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XX 07-JUN-2000; 2000US-0209467P.
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XX 28-JUN-2000; 2000US-0214886P.
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XX 11-JUL-2000; 2000US-0217496P.
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XX 02-OCT-2000; 2000US-0237040P.
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PR 20-OCT-2000; 2000US-0241221P.
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 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
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 PR 08-NOV-2000; 2000US-0246525P.
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 PR 08-NOV-2000; 2000US-0246610P.
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 PR 17-NOV-2000; 2000US-0249213P.
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 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
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 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
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 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0251990P.
 PR 05-JAN-2001; 2001US-0254097P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI; 2001-483426/52.
 DR P-PSDB; AAM85955.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 ES Claim 1; SEQ ID NO 3796; 3071pp + Sequence Listing; English.
 CC
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 109 BP; 26 A; 29 C; 30 G; 23 T; 0 U; 1 Other;

Query Match 3.6%; Score 18; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 TTGCCAGCGGAGTGGTGA 241
 |||||
 DB 51 TTGCCAGCGGAGTGGTGA 68

RESULT 14
 ADE81992
 ID ADE81992 standard; cDNA; 487 BP.
 XX
 AC ADE81992;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Arabidopsis thaliana expressed polynucleotide seq id 763.
 XX
 KW genetically modified organism; transgenic organism; plant;
 KW inhibitor testing; activator testing; modifier testing; fungicide;
 KW insecticide; genetic function; genetic regulation; cellular metabolism;
 KW gene; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 PN US2003115639-A1.
 XX
 PD 19-JUN-2003.
 XX
 PF 26-JAN-2001; 2001US-00770961.
 XX
 PR 27-JAN-2000; 2000US-0178466P.
 XX
 PA (GORL/) GORLACH J.
 PA (ANY/) AN Y.
 PA (HAMI/) HAMILTON C M.
 PA (PRIC/) PRICE J L.
 PA (RAIN/) RAINES T M.
 PA (YUY/) YU Y.
 PA (RAME/) RAMEAKA J G.
 PA (PAGE/) PAGE A.
 PA (MATH/) MATHW A V.
 PA (LEDF/) LEDFORD B L.
 PA (WOES/) WOESSNER J P.
 PA (HAAS/) HAAS W D.
 PA (GARC/) GARCIA C A.
 PA (KEIC/) KRICKER M.
 PA (SLAT/) SLATER T.
 PA (DAVI/) DAVIS K R.
 PA (ALLE/) ALLEN K.
 PA (HOFF/) HOFFMAN N.
 PA (HURB/) HURBAN P.
 XX
 XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;

PI Hurban P;
 XX WPI; 2003-810930/76.
 XX
 PT Novel Arabidopsis thaliana nucleic acids useful for generating
 PT genetically modified transgenic organisms, for screening biologically
 PT active agents such as fungicides, insecticides.
 XX
 PS Claim 1; SEQ ID NO 763; 44pp; English.
 XX
 CC The invention describes a nucleic acid (I) comprising a sequence capable
 CC of hybridising under stringent conditions to any one of 999 fully defined
 CC Arabidopsis thaliana sequences (I) as given in specification e.g., 360,
 CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (I) is useful as a
 CC hybridisation probe to complementary molecules in a cDNA library. (I) is
 CC also useful for generating genetically modified and transgenic organisms,
 CC usually plant cells and plants. A protein encoded by (I) is useful in
 CC screening assays to determine the effect of candidate inhibitors,
 CC activators or modifiers of the gene product. The protein is also useful
 CC for screening biologically active agents e.g., fungicides and
 CC insecticides. A genetically modified cell, comprising an exogenous
 CC nucleic acid, where the nucleic acid comprises transcription regulatory
 CC sequences operably linked to a sequence capable of hybridising under
 CC stringent conditions to (I) is useful in the study of genetic function
 CC and regulation, for alteration of the cellular metabolism and for
 CC screening compounds that may affect the biological function of the gene
 CC or gene product. This sequence represents an Arabidopsis thaliana
 CC polynucleotide of the invention.
 XX
 SQ Sequence 487 BP; 109 A; 132 C; 96 G; 150 T; 0 U; 0 Other;
 Query Match 3.6%; Score 18; DB 9; Length 487;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 430 CAAGCTCTTCTGATTTT 447
 Db 467 CAAGCTCTTCTGATTTT 484
 RESULT 15
 ACH25364/c
 ID ACH25364 standard; cDNA; 584 BP.
 XX
 AC ACH25364;
 XX
 DT 13-OCT-2003 (first entry)
 DE Human adult ovary cDNA #3744.
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX Homo sapiens.
 OS
 XX US2003073623-A1.
 PN 17-APR-2003.
 PD
 XX 30-JUL-2001; 2001US-00918995.
 PF
 XX 30-JUL-2001; 2001US-00918995.
 PR
 XX (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 DR
 XX

PT New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 PS Claim 1; SEQ ID NO 12576; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX
 SQ Sequence 584 BP; 158 A; 128 C; 122 G; 168 T; 0 U; 8 Other;
 Query Match 3.6%; Score 18; DB 8; Length 584;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 302 TTCTGCAGGGCATAGATT 319
 Db 475 TTCTGCAGGGCATAGATT 458
 Search completed: August 4, 2004, 14:34:52
 Job time : 353 secs

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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 14:23:12 ; Search time 65 Seconds
(without alignments)
4268.853 Million cell updates/sec

Title: US-09-987-763-7
Perfect score: 500
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	17	3.4	1243	US-09-103-875-16	Sequence 16, Appl
C 3	17	3.4	1813	US-09-023-655-407	Sequence 407, Appl
C 4	17	3.4	7055	US-09-976-594-941	Sequence 941, Appl
C 5	17	3.4	11443	US-08-961-527-49	Sequence 49, Appl
C 6	17	3.4	28473	US-08-961-527-83	Sequence 83, Appl
C 7	17	3.4	786431	US-09-751-389-3	Sequence 3, Appl
C 8	16	3.2	201	US-09-621-976-13504	Sequence 13504, A
C 9	16	3.2	471	US-09-252-991A-4718	Sequence 4718, Ap
C 10	16	3.2	494	US-09-621-976-2247	Sequence 2247, Ap
C 11	16	3.2	612	US-09-252-991A-4793	Sequence 4793, Ap
C 12	16	3.2	657	US-09-252-991A-14857	Sequence 14857, A
C 13	16	3.2	795	US-08-969-644-15	Sequence 15, Appl
C 14	16	3.2	795	US-08-444-189-15	Sequence 15, Appl
C 15	16	3.2	915	US-08-468-544-15	Sequence 15, Appl
C 16	16	3.2	954	US-09-621-976-1179	Sequence 1179, Ap
C 17	16	3.2	954	US-09-252-991A-4820	Sequence 4820, Ap
C 18	16	3.2	1005	US-09-647-224A-5	Sequence 5, Appl
C 19	16	3.2	1037	US-09-535-008-57	Sequence 57, Appl
C 20	16	3.2	1059	US-09-134-000C-1838	Sequence 1838, Ap
C 21	16	3.2	1110	US-09-107-532A-1616	Sequence 1616, Ap
C 22	16	3.2	1164	US-09-252-991A-14503	Sequence 14503, A
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C 24	16	3.2	1539	US-09-107-532A-2905	Sequence 2905, Ap
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c 102	15	3.0	686	3	US-08-953-326-21	Sequence 21, Appl	c 175	15	3.0	3105	4	US-09-252-991A-10087	Sequence 10087, A
c 103	15	3.0	686	4	US-09-553-662-21	Sequence 21, Appl	c 176	15	3.0	3276	4	US-09-149-476-298	Sequence 298, App
c 104	15	3.0	686	4	US-10-062-994-21	Sequence 21, Appl	c 177	15	3.0	3435	4	US-09-252-991A-10017	Sequence 10017, A
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c 106	15	3.0	699	3	US-08-998-416-815	Sequence 815, App	c 179	15	3.0	3702	4	US-09-252-991A-6666	Sequence 6666, Ap
c 107	15	3.0	702	4	US-09-543-681A-3789	Sequence 3789, App	c 180	15	3.0	3725	1	US-08-155-331-12	Sequence 12, Appl
c 108	15	3.0	718	3	US-08-998-416-890	Sequence 890, App	c 181	15	3.0	3725	1	US-08-424-022-12	Sequence 12, Appl
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c 114	15	3.0	894	4	US-08-328-352-3915	Sequence 3915, App	c 187	15	3.0	5000	4	US-09-302-769-45	Sequence 45, Appl
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c 117	15	3.0	936	4	US-09-543-681A-1605	Sequence 1605, App	c 190	15	3.0	6220	4	US-09-600-087-1	Sequence 1, Appli
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c 142	15	3.0	1542	4	US-09-252-991A-10809	Sequence 10809, A	c 215	15	3.0	169998	4	US-09-676-610B-24	Sequence 24, Appl
c 143	15	3.0	1553	3	US-08-492-459-21	Sequence 21, Appl	c 216	15	3.0	179496	4	US-09-877-177A-10	Sequence 10, Appl
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c 145	15	3.0	1553	3	US-08-716-873-35	Sequence 35, Appl	c 218	15	3.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
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c 155	15	3.0	2040	3	US-08-581-148C-21	Sequence 21, Appl	c 228	15	3.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
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c 158	15	3.0	2274	3	US-08-492-459-13	Sequence 13, Appl	c 231	14	2.8	32	2	US-08-586-676E-13	Sequence 13, Appl
c 159	15	3.0	2274	3	US-08-423-752-13	Sequence 13, Appl	c 232	14	2.8	42	1	US-08-331-398A-26	Sequence 26, Appl
c 160	15	3.0	2274	3	US-08-716-873-27	Sequence 27, Appl	c 233	14	2.8	42	2	US-08-331-397B-26	Sequence 26, Appl
c 161	15	3.0	2274	3	US-09-368-431-27	Sequence 27, Appl	c 234	14	2.8	42	2	US-08-759-804A-26	Sequence 26, Appl
c 162	15	3.0	2274	4	US-09-414-006-13	Sequence 13, Appl	c 235	14	2.8	42	3	US-09-227-693-26	Sequence 26, Appl
c 163	15	3.0	2274	4	US-09-414-006-13	Sequence 13, Appl	c 236	14	2.8	45	2	US-08-184-009-91	Sequence 91, Appl
c 164	15	3.0	2349	4	US-09-252-991A-4983	Sequence 4983, App	c 237	14	2.8	45	2	US-08-458-356-91	Sequence 91, Appl
c 165	15	3.0	2419	4	US-09-624-693A-12	Sequence 12, Appl	c 238	14	2.8	45	3	US-08-796-101-162	Sequence 162, App
c 166	15	3.0	2457	4	US-09-328-352-1082	Sequence 1082, App	c 239	14	2.8	45	3	US-08-460-736-91	Sequence 91, Appl
c 167	15	3.0	2539	3	US-08-581-148C-20	Sequence 20, Appl	c 240	14	2.8	45	4	US-09-535-370-91	Sequence 91, Appl
c 168	15	3.0	2539	3	US-09-620-312D-454	Sequence 454, App	c 241	14	2.8	48	1	US-08-208-886C-77	Sequence 77, Appl
c 169	15	3.0	2572	3	US-08-976-255-1	Sequence 1, Appli	c 242	14	2.8	48	1	US-08-704-744-77	Sequence 77, Appl
c 170	15	3.0	2684	1	US-08-367-227-1	Sequence 1, Appli	c 243	14	2.8	51	4	US-09-029-228-7	Sequence 7, Appl
c 171	15	3.0	2686	3	US-08-952-365-5	Sequence 5, Appli	c 244	14	2.8	52	1	US-08-208-886C-78	Sequence 78, Appl
c 172	15	3.0	2932	3	US-08-999-774A-5	Sequence 5, Appli	c 245	14	2.8	52	1	US-08-704-744-78	Sequence 78, Appl
c 173	15	3.0	2933	4	US-09-149-476-165	Sequence 165, App	c 246	14	2.8	79	3	US-09-449-293-2	Sequence 2, Appli

c 247	14	2.8	79	4	US-09-775-325-2	Sequence 2, Appli	c 320	14	2.8	543	4	US-09-671-325-1394	Sequence 1394, Ap
c 248	14	2.8	79	4	US-09-775-174-2	Sequence 2, Appli	321	14	2.8	544	4	US-09-634-238-147	Sequence 147, App
c 249	14	2.8	126	3	US-08-905-223-67	Sequence 67, Appl	322	14	2.8	546	4	US-09-621-976-2129	Sequence 2129, Ap
c 250	14	2.8	130	1	US-08-305-699-9	Sequence 9, Appli	323	14	2.8	550	4	US-09-669-751-226	Sequence 226, App
c 251	14	2.8	137	1	US-08-299-498A-19	Sequence 19, Appl	324	14	2.8	555	4	US-09-552-322-9	Sequence 9, Appli
c 252	14	2.8	137	5	PCT-US95-10813-19	Sequence 19, Appl	325	14	2.8	558	4	US-09-252-991A-14289	Sequence 14289, A
c 253	14	2.8	154	2	US-08-533-996A-1	Sequence 1, Appli	326	14	2.8	562	5	PCT-US92-03993-6	Sequence 6, Appli
c 254	14	2.8	178	3	US-08-991-789A-210	Sequence 210, App	327	14	2.8	564	4	US-09-252-991A-1261	Sequence 1261, Ap
c 255	14	2.8	178	4	US-09-621-976-210	Sequence 210, App	328	14	2.8	568	4	US-09-621-976-1733	Sequence 1733, Ap
c 256	14	2.8	178	4	US-09-598-326-210	Sequence 210, App	329	14	2.8	570	1	US-07-822-966B-1	Sequence 1, Appli
c 257	14	2.8	178	4	US-09-289-198-210	Sequence 210, App	330	14	2.8	578	3	US-09-328-111-742	Sequence 742, App
c 258	14	2.8	178	4	US-09-429-755-210	Sequence 210, App	331	14	2.8	604	4	US-09-342-653-3	Sequence 3, Appli
c 259	14	2.8	185	3	US-08-480-640A-156	Sequence 156, App	332	14	2.8	609	4	US-09-252-991A-8982	Sequence 8982, Ap
c 260	14	2.8	185	3	US-08-295-802-156	Sequence 156, App	333	14	2.8	627	3	US-08-361-441B-4	Sequence 4, Appli
c 261	14	2.8	185	3	US-08-488-237A-156	Sequence 156, App	334	14	2.8	628	4	US-09-221-017B-79	Sequence 79, Appl
c 262	14	2.8	185	4	US-08-375-992A-156	Sequence 156, App	335	14	2.8	633	4	US-09-252-991A-8508	Sequence 8508, Ap
c 263	14	2.8	185	4	US-08-472-679H-156	Sequence 156, App	336	14	2.8	636	4	US-09-489-039A-2437	Sequence 2437, Ap
c 264	14	2.8	196	4	US-09-313-294A-5796	Sequence 5796, Ap	337	14	2.8	646	4	US-09-016-434-1385	Sequence 1385, Ap
c 265	14	2.8	198	4	US-09-328-352-3145	Sequence 3145, Ap	338	14	2.8	651	1	US-08-171-385-4	Sequence 4, Appli
c 266	14	2.8	198	4	US-09-328-352-3560	Sequence 3560, Ap	339	14	2.8	654	4	US-09-252-991A-2446	Sequence 2446, Ap
c 267	14	2.8	218	4	US-09-506-729-61	Sequence 61, Appl	340	14	2.8	654	4	US-09-252-991A-12606	Sequence 12606, A
c 268	14	2.8	221	3	US-09-060-756-584	Sequence 584, App	341	14	2.8	654	4	US-09-328-352-1232	Sequence 1232, Ap
c 269	14	2.8	221	4	US-09-670-314-584	Sequence 584, App	342	14	2.8	666	4	US-09-543-681A-147	Sequence 147, App
c 270	14	2.8	234	4	US-09-489-039A-3210	Sequence 3210, Ap	343	14	2.8	678	2	US-08-951-871-3	Sequence 3, Appli
c 271	14	2.8	237	4	US-09-489-039A-5342	Sequence 5342, Ap	344	14	2.8	678	4	US-09-107-532A-1586	Sequence 1586, Ap
c 272	14	2.8	271	4	US-09-313-294A-5134	Sequence 5134, Ap	345	14	2.8	681	4	US-09-328-352-1437	Sequence 1437, Ap
c 273	14	2.8	276	4	US-09-252-991A-15626	Sequence 15626, A	346	14	2.8	696	4	US-09-489-039A-2440	Sequence 2440, Ap
c 274	14	2.8	278	4	US-09-621-976-10330	Sequence 10330, A	347	14	2.8	699	4	US-09-252-991A-4020	Sequence 4020, Ap
c 275	14	2.8	285	4	US-09-252-991A-11646	Sequence 11646, A	348	14	2.8	699	4	US-09-252-991A-14260	Sequence 14260, A
c 276	14	2.8	288	3	US-09-025-151-29	Sequence 29, Appl	349	14	2.8	707	3	US-08-998-416-876	Sequence 876, App
c 277	14	2.8	288	4	US-09-637-240-29	Sequence 29, Appl	350	14	2.8	720	4	US-09-252-991A-8875	Sequence 8875, Ap
c 278	14	2.8	293	4	US-09-313-294A-4949	Sequence 4949, Ap	351	14	2.8	720	4	US-09-489-039A-396	Sequence 396, App
c 279	14	2.8	310	4	US-09-313-294A-6506	Sequence 6506, Ap	352	14	2.8	720	4	US-09-134-000C-32	Sequence 32, Appl
c 280	14	2.8	315	4	US-09-489-039A-5096	Sequence 5096, Ap	353	14	2.8	724	4	US-09-328-475C-291	Sequence 291, App
c 281	14	2.8	321	4	US-09-252-991A-4442	Sequence 4442, Ap	354	14	2.8	729	4	US-09-252-991A-11790	Sequence 11790, A
c 282	14	2.8	322	1	US-09-985-799-61	Sequence 61, Appl	355	14	2.8	736	3	US-08-998-416-875	Sequence 875, App
c 283	14	2.8	322	1	US-08-594-031-61	Sequence 61, Appl	356	14	2.8	740	4	US-09-328-475C-290	Sequence 290, App
c 284	14	2.8	330	4	US-09-341-444A-3	Sequence 3, Appli	357	14	2.8	741	4	US-09-134-001C-1950	Sequence 1950, Ap
c 285	14	2.8	334	4	US-09-453-702B-80	Sequence 80, Appl	358	14	2.8	741	4	US-09-252-991A-11040	Sequence 11040, A
c 286	14	2.8	361	4	US-09-590-759-110	Sequence 110, App	359	14	2.8	744	4	US-09-540-236-987	Sequence 987, App
c 287	14	2.8	383	4	US-09-636-215-693	Sequence 693, App	360	14	2.8	746	4	US-09-902-331B-15	Sequence 15, Appl
c 288	14	2.8	383	4	US-09-685-166A-693	Sequence 693, App	361	14	2.8	748	3	US-09-154-083-1	Sequence 1, Appli
c 289	14	2.8	384	4	US-09-590-759-111	Sequence 111, App	362	14	2.8	750	4	US-09-489-039A-5270	Sequence 5270, Ap
c 290	14	2.8	384	4	US-09-392-184-23	Sequence 23, Appl	363	14	2.8	753	3	US-09-154-083-28	Sequence 28, Appl
c 291	14	2.8	404	1	US-09-985-799-154	Sequence 154, App	364	14	2.8	753	4	US-09-489-039A-1736	Sequence 1736, Ap
c 292	14	2.8	404	1	US-08-594-031-154	Sequence 154, App	365	14	2.8	759	4	US-09-769-482-2	Sequence 2, Appli
c 293	14	2.8	410	4	US-09-341-444A-1	Sequence 1, Appli	366	14	2.8	762	4	US-09-252-991A-7992	Sequence 7992, Ap
c 294	14	2.8	426	4	US-08-956-171E-694	Sequence 694, App	367	14	2.8	763	4	US-09-976-594-1070	Sequence 1070, Ap
c 295	14	2.8	435	1	US-08-208-886C-79	Sequence 79, Appl	368	14	2.8	769	4	US-08-858-207A-146	Sequence 146, App
c 296	14	2.8	435	1	US-08-704-744-79	Sequence 79, Appl	369	14	2.8	771	4	US-09-489-039A-5488	Sequence 5488, Ap
c 297	14	2.8	441	4	US-09-134-000C-1585	Sequence 1585, Ap	370	14	2.8	789	4	US-09-702-705-214	Sequence 214, App
c 298	14	2.8	447	4	US-09-252-991A-11703	Sequence 11703, A	371	14	2.8	789	4	US-09-736-457-214	Sequence 214, App
c 299	14	2.8	450	4	US-09-252-991A-8210	Sequence 8210, Ap	372	14	2.8	789	4	US-09-489-039A-4757	Sequence 4757, Ap
c 300	14	2.8	450	4	US-09-252-991A-12041	Sequence 12041, A	373	14	2.8	789	4	US-09-614-124B-214	Sequence 214, App
c 301	14	2.8	451	4	US-09-621-976-16268	Sequence 16268, A	374	14	2.8	789	4	US-09-671-325-214	Sequence 214, App
c 302	14	2.8	457	4	US-09-621-976-16364	Sequence 16364, A	375	14	2.8	789	4	US-09-589-184-214	Sequence 214, App
c 303	14	2.8	468	4	US-09-621-976-2410	Sequence 2410, Ap	376	14	2.8	801	4	US-09-543-681A-2922	Sequence 2922, Ap
c 304	14	2.8	478	4	US-09-621-976-10978	Sequence 10978, A	377	14	2.8	807	4	US-09-328-352-455	Sequence 455, App
c 305	14	2.8	478	4	US-09-621-976-13008	Sequence 13008, A	378	14	2.8	807	4	US-09-107-532A-2403	Sequence 2403, Ap
c 306	14	2.8	484	4	US-09-643-597-198	Sequence 198, App	379	14	2.8	819	4	US-09-489-039A-3592	Sequence 3592, Ap
c 307	14	2.8	484	4	US-09-480-884A-198	Sequence 198, App	380	14	2.8	834	4	US-09-134-000C-753	Sequence 753, App
c 308	14	2.8	484	4	US-09-542-615A-198	Sequence 198, App	381	14	2.8	845	2	US-08-266-451B-1	Sequence 1, Appli
c 309	14	2.8	484	4	US-09-606-421B-198	Sequence 198, App	382	14	2.8	845	2	US-08-748-725-1	Sequence 1, Appli
c 310	14	2.8	486	4	US-09-621-976-3282	Sequence 3282, Ap	383	14	2.8	846	4	US-09-252-991A-8327	Sequence 8327, Ap
c 311	14	2.8	487	4	US-08-956-171E-547	Sequence 547, App	384	14	2.8	851	3	US-08-998-416-294	Sequence 294, App
c 312	14	2.8	520	4	US-09-621-976-767	Sequence 767, App	385	14	2.8	854	4	US-09-401-064-329	Sequence 329, App
c 313	14	2.8	525	4	US-09-833-381-945	Sequence 945, App	386	14	2.8	860	4	US-09-833-381-303	Sequence 303, App
c 314	14	2.8	535	4	US-09-833-381-560	Sequence 560, App	387	14	2.8	870	4	US-08-956-171E-879	Sequence 879, App
c 315	14	2.8	537	4	US-09-976-594-135	Sequence 135, App	388	14	2.8	886	4	US-09-325-932A-94	Sequence 94, Appl
c 316	14	2.8	543	4	US-09-702-705-1394	Sequence 1394, Ap	389	14	2.8	891	4	US-09-535-909-13	Sequence 13, Appl
c 317	14	2.8	543	4	US-09-736-457-1394	Sequence 1394, Ap	390	14	2.8	891	4	US-09-543-681A-204	Sequence 204, App
c 318	14	2.8	543	4	US-09-134-000C-1295	Sequence 1295, Ap	391	14	2.8	891	4	US-09-543-681A-1919	Sequence 1919, Ap
c 319	14	2.8	543	4	US-09-614-124B-1394	Sequence 1394, Ap	392	14	2.8	891	4	US-09-540-236-923	Sequence 923, App

393	14	2.8	894	4	US-09-252-991A-6276	Sequence 6276, Ap	c 466	14	2.8	1446	4	US-09-252-991A-11593	Sequence 11593, A
394	14	2.8	900	4	US-09-050-739-65	Sequence 65, Appl	467	14	2.8	1451	4	US-09-489-039A-5036	Sequence 5036, Ap
C 395	14	2.8	915	4	US-09-489-039A-5405	Sequence 5405, Ap	C 468	14	2.8	1458	4	US-09-134-000C-987	Sequence 987, App
C 396	14	2.8	917	4	US-09-976-594-483	Sequence 483, App	C 469	14	2.8	1464	4	US-09-107-532A-1565	Sequence 1565, Ap
C 397	14	2.8	921	4	US-09-023-555-401	Sequence 401, App	C 470	14	2.8	1473	4	US-09-252-991A-2391	Sequence 2391, Ap
C 398	14	2.8	944	4	US-09-071-035-379	Sequence 379, App	C 471	14	2.8	1494	4	US-09-535-909-2	Sequence 2, Appli
C 399	14	2.8	961	5	PCT-US91-08177-14	Sequence 14, Appl	C 472	14	2.8	1512	4	US-09-543-681A-39	Sequence 39, Appl
C 400	14	2.8	978	4	US-09-252-991A-13988	Sequence 13988, A	C 473	14	2.8	1519	4	US-10-024-427-3	Sequence 32, Appl
C 401	14	2.8	1001	4	US-09-671-317-89	Sequence 89, Appl	C 474	14	2.8	1521	4	US-09-540-236-322	Sequence 322, Ap
C 402	14	2.8	1002	4	US-09-252-991A-11214	Sequence 11214, A	C 475	14	2.8	1524	4	US-09-252-991A-6970	Sequence 6970, Ap
C 403	14	2.8	1005	4	US-09-134-000C-337	Sequence 337, App	C 476	14	2.8	1528	2	US-08-945-296-3	Sequence 3, Appli
C 404	14	2.8	1029	4	US-09-540-236-1285	Sequence 1285, Ap	C 477	14	2.8	1538	4	US-09-405-112-3	Sequence 3, Appli
C 405	14	2.8	1032	4	US-09-266-965-33	Sequence 33, Appl	C 478	14	2.8	1536	4	US-09-489-039A-7086	Sequence 7086, Ap
C 406	14	2.8	1035	4	US-09-489-039A-2467	Sequence 2467, Ap	C 479	14	2.8	1546	4	US-09-383-318A-1	Sequence 1, Appli
C 407	14	2.8	1035	4	US-09-134-000C-1789	Sequence 1789, App	C 480	14	2.8	1551	4	US-09-543-681A-1213	Sequence 1213, Ap
C 408	14	2.8	1038	4	US-09-540-236-1341	Sequence 1341, Ap	C 481	14	2.8	1566	4	US-09-252-991A-8520	Sequence 8520, Ap
C 409	14	2.8	1050	4	US-09-252-991A-6362	Sequence 6362, Ap	C 482	14	2.8	1575	3	US-09-230-388-2	Sequence 2, Appli
C 410	14	2.8	1053	4	US-09-107-532A-2650	Sequence 2650, Ap	C 483	14	2.8	1575	4	US-09-912-176-2	Sequence 2, Appli
C 411	14	2.8	1068	4	US-09-134-000C-808	Sequence 808, App	C 484	14	2.8	1588	1	US-08-706-037-24	Sequence 24, Appl
C 412	14	2.8	1080	4	US-09-328-352-2971	Sequence 2971, Ap	C 485	14	2.8	1588	2	US-09-005-397-24	Sequence 6324, Ap
C 413	14	2.8	1086	4	US-09-134-000C-1759	Sequence 1759, App	C 486	14	2.8	1611	4	US-09-252-991A-6924	Sequence 6729, Ap
C 414	14	2.8	1089	4	US-09-071-035-377	Sequence 377, App	C 487	14	2.8	1623	4	US-09-252-991A-9839	Sequence 9839, Ap
C 415	14	2.8	1090	3	US-09-124-758-1	Sequence 1, Appli	C 488	14	2.8	1623	4	US-09-252-991A-9839	Sequence 4, Appli
C 416	14	2.8	1090	4	US-09-768-677-1	Sequence 1, Appli	C 489	14	2.8	1635	3	US-09-234-332-4	Sequence 1798, Ap
C 417	14	2.8	1107	4	US-09-252-991A-456	Sequence 456, App	C 490	14	2.8	1635	4	US-09-702-705-1798	Sequence 1798, Ap
C 418	14	2.8	1122	4	US-09-134-000C-1964	Sequence 1964, Ap	C 491	14	2.8	1635	4	US-09-736-457-1798	Sequence 1798, Ap
C 419	14	2.8	1125	4	US-09-540-236-310	Sequence 310, App	C 492	14	2.8	1635	4	US-09-671-325-1798	Sequence 1798, Ap
C 420	14	2.8	1134	4	US-09-622-439-21	Sequence 21, Appl	C 493	14	2.8	1647	4	US-09-107-532A-2973	Sequence 2973, Ap
C 421	14	2.8	1134	4	US-09-491-577-83	Sequence 83, Appl	C 494	14	2.8	1665	4	US-09-252-991A-14320	Sequence 14320, A
C 422	14	2.8	1137	4	US-09-540-236-763	Sequence 763, App	C 495	14	2.8	1671	4	US-09-543-681A-1663	Sequence 1663, Ap
C 423	14	2.8	1140	4	US-09-769-482-1	Sequence 1, Appli	C 496	14	2.8	1672	1	US-08-172-331B-13	Sequence 13, Appl
C 424	14	2.8	1151	3	US-09-221-298-8	Sequence 8, Appli	C 497	14	2.8	1677	4	US-09-328-352-1861	Sequence 1861, Ap
C 425	14	2.8	1154	4	US-09-616-382A-1	Sequence 8, Appli	C 498	14	2.8	1695	5	PCT-US96-05320A-265	Sequence 265, App
C 426	14	2.8	1154	4	US-09-540-236-1516	Sequence 1516, Ap	C 499	14	2.8	1713	4	US-09-252-991A-109	Sequence 109, App
C 427	14	2.8	1176	2	US-08-923-856-2	Sequence 2, Appli	C 500	14	2.8	1713	4	US-09-489-039A-157	Sequence 157, App
C 428	14	2.8	1176	4	US-09-216-294-2	Sequence 2, Appli	C 501	14	2.8	1782	4	US-09-252-991A-6769	Sequence 6769, Ap
C 429	14	2.8	1212	4	US-09-489-039A-5241	Sequence 5241, Ap	C 502	14	2.8	1782	4	US-09-252-991A-15714	Sequence 15714, A
C 430	14	2.8	1218	4	US-09-489-039A-42	Sequence 42, Appl	C 503	14	2.8	1790	4	US-09-133-962A-7	Sequence 7, Appli
C 431	14	2.8	1218	4	US-09-252-991A-2125	Sequence 2125, Ap	C 504	14	2.8	1794	4	US-09-252-991A-5181	Sequence 5181, Ap
C 432	14	2.8	1221	4	US-09-328-352-3564	Sequence 3564, Ap	C 505	14	2.8	1806	4	US-09-252-991A-2306	Sequence 2306, Ap
C 433	14	2.8	1221	4	US-08-956-171E-13	Sequence 13, Appl	C 506	14	2.8	1811	4	US-09-535-909-3	Sequence 3, Appli
C 434	14	2.8	1222	4	US-09-784-990-22	Sequence 22, Appl	C 507	14	2.8	1822	4	US-09-833-381-1063	Sequence 1063, Ap
C 435	14	2.8	1230	3	US-09-232-479-22	Sequence 22, Appl	C 508	14	2.8	1843	4	US-09-807-258-3	Sequence 3, Appli
C 436	14	2.8	1230	4	US-09-784-990-22	Sequence 22, Appl	C 509	14	2.8	1896	4	US-09-134-000C-2770	Sequence 2770, Ap
C 437	14	2.8	1242	4	US-09-799-978-31	Sequence 31, Appl	C 510	14	2.8	1908	1	US-08-173-508-1	Sequence 1, Appli
C 438	14	2.8	1248	4	US-09-252-991A-9193	Sequence 9193, Ap	C 511	14	2.8	1908	1	US-08-173-508-1	Sequence 1, Appli
C 439	14	2.8	1251	3	US-09-007-476-1	Sequence 1, Appli	C 512	14	2.8	1908	2	US-08-265-310-1	Sequence 1, Appli
C 440	14	2.8	1251	4	US-09-620-312D-947	Sequence 947, App	C 513	14	2.8	1908	2	US-08-265-310-1	Sequence 1, Appli
C 441	14	2.8	1257	4	US-09-252-991A-14147	Sequence 14147, A	C 514	14	2.8	1908	3	US-08-951-742-1	Sequence 1, Appli
C 442	14	2.8	1260	4	US-09-252-991A-11855	Sequence 11855, A	C 515	14	2.8	1908	3	US-09-220-132-1	Sequence 1, Appli
C 443	14	2.8	1275	4	US-09-252-991A-516	Sequence 516, App	C 516	14	2.8	1931	4	US-09-232-191-32	Sequence 32, Appl
C 444	14	2.8	1278	4	US-10-024-427-1	Sequence 1, Appli	C 517	14	2.8	1932	3	US-09-232-200-82	Sequence 82, Appl
C 445	14	2.8	1284	4	US-09-894-844-106	Sequence 106, App	C 518	14	2.8	1932	3	US-09-232-197-82	Sequence 82, Appl
C 446	14	2.8	1287	4	US-09-134-000C-3052	Sequence 3052, Ap	C 519	14	2.8	1932	4	US-09-232-201-82	Sequence 82, Appl
C 447	14	2.8	1317	4	US-09-252-991A-11011	Sequence 11011, A	C 520	14	2.8	1932	4	US-09-232-195-82	Sequence 82, Appl
C 448	14	2.8	1322	4	US-09-579-236-3	Sequence 3, Appli	C 521	14	2.8	1934	4	US-09-579-236-1	Sequence 1, Appli
C 449	14	2.8	1326	4	US-09-252-991A-409	Sequence 409, App	C 522	14	2.8	1945	3	US-08-714-918-77	Sequence 77, Appl
C 450	14	2.8	1331	4	US-09-976-594-702	Sequence 702, App	C 523	14	2.8	1945	3	US-09-265-315-77	Sequence 77, Appl
C 451	14	2.8	1333	3	US-09-142-551A-1	Sequence 1, Appli	C 524	14	2.8	1945	3	US-09-265-315-77	Sequence 77, Appl
C 452	14	2.8	1338	4	US-08-887-534A-60	Sequence 60, Appl	C 525	14	2.8	1945	3	US-09-266-417-77	Sequence 77, Appl
C 453	14	2.8	1338	4	US-08-527-431-60	Sequence 60, Appl	C 526	14	2.8	1945	3	US-09-528-709-77	Sequence 77, Appl
C 454	14	2.8	1344	4	US-09-252-991A-5239	Sequence 5239, Ap	C 527	14	2.8	1945	4	US-09-527-745-77	Sequence 77, Appl
C 455	14	2.8	1345	4	US-09-976-594-239	Sequence 239, App	C 528	14	2.8	1964	1	US-08-132-168A-31	Sequence 31, Appl
C 456	14	2.8	1353	4	US-09-252-991A-3984	Sequence 3984, Ap	C 529	14	2.8	1995	4	US-09-107-532A-3598	Sequence 3598, Ap
C 457	14	2.8	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	C 530	14	2.8	1995	4	US-09-252-991A-6189	Sequence 6189, Ap
C 458	14	2.8	1371	4	US-09-976-594-608	Sequence 608, App	C 531	14	2.8	1998	4	US-09-252-991A-8142	Sequence 8142, Ap
C 459	14	2.8	1386	4	US-09-489-039A-4802	Sequence 4802, Ap	C 532	14	2.8	2031	4	US-09-328-352-3700	Sequence 3700, Ap
C 460	14	2.8	1392	5	PCT-US96-05320A-300	Sequence 300, App	C 533	14	2.8	2034	4	US-09-252-991A-11782	Sequence 11782, A
C 461	14	2.8	1401	4	US-09-252-991A-10908	Sequence 10908, A	C 534	14	2.8	2118	4	US-09-164-034B-1	GENERAL INFORMA
C 462	14	2.8	1401	4	US-09-543-681A-531	Sequence 531, App	C 535	14	2.8	2133	4	US-09-747-259-15	Sequence 15, Appl
C 463	14	2.8	1422	4	US-09-134-000C-2035	Sequence 2035, Ap	C 536	14	2.8	2138	4	US-09-784-651-3	Sequence 3, Appli
C 464	14	2.8	1425	4	US-09-252-991A-11848	Sequence 11848, A	C 537	14	2.8	2149	1	US-08-747-651-3	Sequence 294, App
C 465	14	2.8	1435	2	US-08-955-713-3	Sequence 3, Appli	C 538	14	2.8	2154	4	US-09-495-050A-294	

539	14	2.8	2168	1	US-08-784-651-1	Sequence 1, Appl	c 612	14	2.8	2865	4	US-09-252-991A-16281	Sequence 16281, A
540	14	2.8	2184	4	US-09-540-236-1103	Sequence 1103, Ap	c 613	14	2.8	2871	4	US-09-489-847-111	Sequence 111, App
541	14	2.8	2191	4	US-09-071-035-363	Sequence 363, App	c 614	14	2.8	2874	4	US-09-252-991A-15997	Sequence 15997, A
542	14	2.8	2200	4	US-09-134-001C-749	Sequence 749, App	c 615	14	2.8	2876	4	US-09-489-847-22	Sequence 22, Appl
543	14	2.8	2234	1	US-08-261-822A-7	Sequence 7, Appl	c 616	14	2.8	2876	4	US-09-543-681A-2235	Sequence 6, Appl
544	14	2.8	2234	5	PCT-US95-07744A-7	Sequence 7, Appl	c 617	14	2.8	2910	1	US-08-375-709-6	Sequence 6, Appl
545	14	2.8	2257	4	US-09-016-434-1300	Sequence 1300, Ap	c 618	14	2.8	2910	1	US-08-752-929-6	Sequence 81, Appl
546	14	2.8	2285	1	US-08-477-674-9	Sequence 9, Appl	c 619	14	2.8	2910	1	US-09-231-899-81	Sequence 81, Appl
547	14	2.8	2285	2	US-08-316-791-9	Sequence 9, Appl	c 620	14	2.8	2928	4	US-09-328-352-638	Sequence 638, App
548	14	2.8	2285	3	US-08-473-673-9	Sequence 9, Appl	c 621	14	2.8	2929	4	US-09-543-084A-31	Sequence 31, Appl
549	14	2.8	2292	4	US-09-107-532A-1177	Sequence 1177, Ap	c 622	14	2.8	2967	4	US-09-694-777A-14	Sequence 14, Appl
550	14	2.8	2331	4	US-09-134-000C-2312	Sequence 2312, Ap	c 623	14	2.8	2973	4	US-09-133-962A-15	Sequence 15, Appl
551	14	2.8	2331	4	US-09-071-035-361	Sequence 361, App	c 624	14	2.8	3001	4	US-09-539-333D-174	Sequence 174, App
552	14	2.8	2339	4	US-08-858-207A-47	Sequence 47, Appl	c 625	14	2.8	3001	4	US-09-539-333D-175	Sequence 175, App
553	14	2.8	2358	1	US-08-339-152A-15	Sequence 15, Appl	c 626	14	2.8	3051	4	US-09-409-604-1	Sequence 1, Appl
554	14	2.8	2358	2	US-08-007-999B-2	Sequence 2, Appl	c 627	14	2.8	3072	4	US-09-221-017B-337	Sequence 337, App
555	14	2.8	2358	2	US-08-689-276A-2	Sequence 2, Appl	c 628	14	2.8	3083	4	US-09-694-777A-2	Sequence 2, Appl
556	14	2.8	2360	1	US-08-145-681-1	Sequence 1, Appl	c 629	14	2.8	3132	4	US-09-252-991A-15639	Sequence 15639, A
557	14	2.8	2360	1	US-08-250-308-1	Sequence 1, Appl	c 630	14	2.8	3136	4	US-09-751-389-1	Sequence 1, Appl
558	14	2.8	2360	2	US-08-453-703-1	Sequence 1, Appl	c 631	14	2.8	3144	2	US-08-687-916-15	Sequence 15, Appl
559	14	2.8	2360	2	US-08-456-106-1	Sequence 1, Appl	c 632	14	2.8	3144	3	US-09-138-614-15	Sequence 15, Appl
560	14	2.8	2360	3	US-08-456-108-1	Sequence 1, Appl	c 633	14	2.8	3145	4	US-09-221-017B-855	Sequence 855, App
561	14	2.8	2360	3	US-09-265-577-1	Sequence 1, Appl	c 634	14	2.8	3162	4	US-09-252-991A-8094	Sequence 8094, Ap
562	14	2.8	2360	3	US-09-633-733-1	Sequence 1, Appl	c 635	14	2.8	3168	2	US-08-659-251-14	Sequence 14, Appl
563	14	2.8	2360	4	US-09-633-733-1	Sequence 1, Appl	c 636	14	2.8	3168	2	US-09-256-490-14	Sequence 14, Appl
564	14	2.8	2360	4	US-09-252-991A-11973	Sequence 1, Appl	c 637	14	2.8	3168	5	PCT-US96-11445-14	Sequence 14, Appl
565	14	2.8	2367	4	US-09-252-991A-16507	Sequence 16507, A	c 638	14	2.8	3193	4	US-09-543-084A-30	Sequence 30, Appl
566	14	2.8	2382	4	US-08-705-477E-100	Sequence 100, App	c 639	14	2.8	3220	4	US-10-004-542-5	Sequence 5, Appl
567	14	2.8	2387	4	US-08-419-810-11	Sequence 11, Appl	c 640	14	2.8	3222	4	US-09-543-084A-29	Sequence 29, Appl
568	14	2.8	2423	3	US-08-419-810-11	Sequence 11, Appl	c 641	14	2.8	3223	1	US-07-980-528-1	Sequence 1, Appl
569	14	2.8	2423	6	5405775-10	Patent No. 5405775	c 642	14	2.8	3233	3	US-08-755-587-43	Sequence 43, Appl
570	14	2.8	2432	1	US-08-078-683A-1	Sequence 1, Appl	c 643	14	2.8	3242	4	US-09-493-914-2	Sequence 2, Appl
571	14	2.8	2432	4	US-08-471-970A-1	Sequence 1, Appl	c 644	14	2.8	3252	4	US-08-476-102A-4	Sequence 4, Appl
572	14	2.8	2437	3	US-08-904-284-6	Sequence 6, Appl	c 645	14	2.8	3252	5	PCT-US96-05320A-714	Sequence 714, App
573	14	2.8	2439	4	US-09-252-991A-1957	Sequence 1957, Ap	c 646	14	2.8	3255	4	US-09-601-198-108	Sequence 108, App
574	14	2.8	2463	4	US-09-614-912-85	Sequence 85, Appl	c 647	14	2.8	3255	4	US-09-252-991A-12013	Sequence 12013, A
575	14	2.8	2481	4	US-09-016-434-1088	Sequence 1088, Ap	c 648	14	2.8	3279	4	US-09-252-991A-11905	Sequence 11905, A
576	14	2.8	2487	4	US-09-252-991A-14985	Sequence 14985, A	c 649	14	2.8	3404	4	US-09-453-702B-94	Sequence 94, Appl
577	14	2.8	2547	4	US-09-252-991A-5294	Sequence 5294, Ap	c 650	14	2.8	3422	3	US-09-586-719-26	Sequence 26, Appl
578	14	2.8	2554	4	US-09-620-312D-377	Sequence 377, App	c 651	14	2.8	3453	3	US-09-139-064-1	Sequence 1, Appl
579	14	2.8	2571	4	US-09-134-001C-2601	Sequence 2601, Ap	c 652	14	2.8	3453	3	US-09-139-064-3	Sequence 3, Appl
580	14	2.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	c 653	14	2.8	3453	3	US-09-139-064-5	Sequence 5, Appl
581	14	2.8	2601	4	US-09-252-991A-11077	Sequence 11077, Ap	c 654	14	2.8	3453	3	US-09-487-370-1	Sequence 1, Appl
582	14	2.8	2610	4	US-09-252-991A-11177	Sequence 11177, A	c 655	14	2.8	3453	3	US-09-487-370-3	Sequence 3, Appl
583	14	2.8	2622	4	US-09-489-039A-4584	Sequence 4584, Ap	c 656	14	2.8	3453	3	US-09-487-370-5	Sequence 5, Appl
584	14	2.8	2652	4	US-09-543-681A-2440	Sequence 2440, Ap	c 657	14	2.8	3462	4	US-09-362-842-7	Sequence 7, Appl
585	14	2.8	2653	1	US-08-325-553-1	Sequence 1, Appl	c 658	14	2.8	3495	1	US-07-828-788A-13	Sequence 13, Appl
586	14	2.8	2653	2	US-08-394-152A-1	Sequence 1, Appl	c 659	14	2.8	3495	3	US-08-356-034-3	Sequence 3, Appl
587	14	2.8	2653	4	US-08-705-477E-1	Sequence 1, Appl	c 660	14	2.8	3495	3	US-08-933-891-3	Sequence 3, Appl
588	14	2.8	2674	4	US-09-817-180-1	Sequence 1, Appl	c 661	14	2.8	3495	4	US-09-521-344-3	Sequence 3, Appl
589	14	2.8	2674	4	US-10-003-295-1	Sequence 1, Appl	c 662	14	2.8	3495	5	PCT-US92-11337-13	Sequence 13, Appl
590	14	2.8	2675	1	US-08-070-165F-5	Sequence 5, Appl	c 663	14	2.8	3495	6	5188960-3	Patent No. 5188960
591	14	2.8	2675	2	US-08-885-418-5	Sequence 5, Appl	c 664	14	2.8	3528	4	US-09-252-991A-8473	Sequence 8473, Ap
592	14	2.8	2681	1	US-08-070-165F-9	Sequence 9, Appl	c 665	14	2.8	3573	4	US-09-252-991A-4903	Sequence 4903, Ap
593	14	2.8	2681	2	US-08-885-418-9	Sequence 9, Appl	c 666	14	2.8	3576	4	US-09-540-236-982	Sequence 982, App
594	14	2.8	2688	4	US-09-489-039A-5328	Sequence 5328, Ap	c 667	14	2.8	3607	4	US-09-563-269-17	Sequence 17, Appl
595	14	2.8	2712	4	US-09-252-991A-8406	Sequence 8406, Ap	c 668	14	2.8	3744	2	US-08-348-353-16	Sequence 16, Appl
596	14	2.8	2723	1	US-08-961-527-273	Sequence 273, App	c 669	14	2.8	3744	3	US-08-465-965-16	Sequence 16, Appl
597	14	2.8	2733	1	US-08-676-967-3	Sequence 3, Appl	c 670	14	2.8	3744	3	US-08-465-966-16	Sequence 16, Appl
598	14	2.8	2733	2	US-08-676-974-3	Sequence 3, Appl	c 671	14	2.8	3747	2	US-09-080-897-1	Sequence 1, Appl
599	14	2.8	2733	2	US-09-098-487-3	Sequence 3, Appl	c 672	14	2.8	3747	3	US-09-323-735-1	Sequence 1, Appl
600	14	2.8	2739	4	US-09-540-236-40	Sequence 40, Appl	c 673	14	2.8	3803	1	US-08-485-618-52	Sequence 52, Appl
601	14	2.8	2758	4	US-09-221-017B-441	Sequence 441, App	c 674	14	2.8	3803	1	US-08-362-652-52	Sequence 52, Appl
602	14	2.8	2788	4	US-09-021-017B-644	Sequence 644, App	c 675	14	2.8	3803	2	US-08-605-672-52	Sequence 52, Appl
603	14	2.8	2797	2	US-09-021-323-2	Sequence 2, Appl	c 676	14	2.8	3803	2	US-08-483-293A-52	Sequence 52, Appl
604	14	2.8	2815	3	US-09-276-531-127	Sequence 127, App	c 677	14	2.8	3803	2	US-08-943-363-52	Sequence 52, Appl
605	14	2.8	2829	4	US-10-004-542-1	Sequence 1, Appl	c 678	14	2.8	3803	3	US-09-193-043-52	Sequence 52, Appl
606	14	2.8	2831	4	US-09-477-135A-117	Sequence 117, App	c 679	14	2.8	3803	4	US-09-688-307A-52	Sequence 52, Appl
607	14	2.8	2852	4	US-09-056-556-203	Sequence 203, App	c 680	14	2.8	3803	4	US-09-350-259-52	Sequence 52, Appl
608	14	2.8	2852	4	US-09-072-596-198	Sequence 198, App	c 681	14	2.8	3833	1	US-08-917-320-18	Sequence 18, Appl
609	14	2.8	2852	4	US-09-072-596-203	Sequence 203, App	c 682	14	2.8	3833	5	PCT-US95-04611A-18	Sequence 18, Appl
610	14	2.8	2855	4	US-09-904-420A-1	Sequence 1, Appl	c 683	14	2.8	3889	2	US-08-648-298-1	Sequence 1, Appl
611	14	2.8	2859	4	US-09-328-352-425	Sequence 425, App	c 684	14	2.8	3896	4	US-09-795-926-44	Sequence 44, Appl

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686	14	2.8	3903	3	US-09-176-320-5	Sequence 5, Appli	c 759	14	2.8	10754	3	US-09-342-353-1	Sequence 1, Appli
687	14	2.8	4026	4	US-09-252-991A-10214	Sequence 10214, A	c 760	14	2.8	10953	4	US-08-956-171B-62	Sequence 62, Appl
688	14	2.8	4039	4	US-09-205-448-7	Sequence 7, Appli	c 761	14	2.8	11049	4	US-10-204-708-21	Sequence 21, Appl
689	14	2.8	4030	4	US-09-543-084A-26	Sequence 26, Appl	c 762	14	2.8	11049	4	US-10-204-708-21	Sequence 21, Appl
690	14	2.8	4061	3	US-08-425-843-1	Sequence 1, Appli	c 763	14	2.8	11219	1	US-07-642-734C-1	Sequence 1, Appli
691	14	2.8	4078	4	US-09-016-434-1120	Sequence 1120, Ap	c 764	14	2.8	11219	3	US-08-439-009A-1	Sequence 1, Appli
692	14	2.8	4080	4	US-09-016-434-1342	Sequence 1342, Ap	765	14	2.8	11272	4	US-09-341-461-1	Sequence 1, Appli
693	14	2.8	4093	4	US-09-543-084A-28	Sequence 28, Appl	766	14	2.8	11340	2	US-08-961-527-147	Sequence 147, App
694	14	2.8	4101	4	US-09-543-084A-27	Sequence 27, Appl	767	14	2.8	11385	2	US-08-639-501-1	Sequence 1, Appli
695	14	2.8	4117	4	US-08-961-527-100	Sequence 100, App	768	14	2.8	11385	3	US-09-044-946-1	Sequence 1, Appli
696	14	2.8	4138	1	US-08-447-411-75	Sequence 75, Appl	769	14	2.8	11385	3	US-09-044-908-1	Sequence 1, Appli
697	14	2.8	4138	2	US-08-662-227-33	Sequence 33, Appl	770	14	2.8	12145	3	US-08-968-563-19	Sequence 19, Appl
698	14	2.8	4138	4	US-09-017-947-33	Sequence 33, Appl	771	14	2.8	12145	3	US-08-969-683A-19	Sequence 19, Appl
699	14	2.8	4138	4	US-09-925-442-33	Sequence 33, Appl	772	14	2.8	12145	4	US-09-369-796-1	Sequence 1, Appli
700	14	2.8	4145	1	US-08-261-822A-15	Sequence 15, Appl	773	14	2.8	12145	4	US-09-307-973A-10	Sequence 10, Appl
701	14	2.8	4145	5	PCT-US95-0774A-15	Sequence 15, Appl	774	14	2.8	12145	4	US-09-641-652-1	Sequence 1, Appli
702	14	2.8	4191	4	US-09-963-137-200	Sequence 200, App	c 775	14	2.8	12835	4	US-08-961-527-141	Sequence 141, App
703	14	2.8	4197	4	US-09-543-681A-1469	Sequence 1469, Ap	c 776	14	2.8	13104	4	US-08-961-527-34	Sequence 34, Appl
704	14	2.8	4206	4	US-09-302-620B-81	Sequence 81, Appl	c 777	14	2.8	15297	4	US-09-817-180-3	Sequence 3, Appli
705	14	2.8	4206	4	US-09-912-161-3	Sequence 3, Appli	c 778	14	2.8	15297	4	US-10-003-295-3	Sequence 3, Appli
706	14	2.8	4206	4	US-09-911-781-2	Sequence 2, Appli	c 779	14	2.8	15378	3	US-08-785-420-1	Sequence 1, Appli
707	14	2.8	4352	4	US-09-620-312D-555	Sequence 555, App	780	14	2.8	15766	3	US-09-338-907-73	Sequence 73, Appl
708	14	2.8	4414	5	PCT-US95-04567-1	Sequence 1, Appli	781	14	2.8	15766	4	US-09-218-207-73	Sequence 73, Appl
709	14	2.8	4436	4	US-09-491-356C-6	Sequence 6, Appli	782	14	2.8	15788	4	US-09-920-759-13	Sequence 13, Appl
710	14	2.8	4495	2	US-08-849-480A-3	Sequence 3, Appli	783	14	2.8	16995	4	US-08-961-527-82	Sequence 82, Appl
711	14	2.8	4530	4	US-09-566-921-134	Sequence 134, App	784	14	2.8	16995	4	US-08-976-259-70	Sequence 70, Appl
712	14	2.8	4656	3	US-09-425-665-1	Sequence 1, Appli	c 785	14	2.8	18331	4	US-09-266-965-96	Sequence 96, Appl
713	14	2.8	4656	4	US-09-685-668-1	Sequence 1, Appli	c 786	14	2.8	18331	2	US-08-487-826B-13	Sequence 13, Appl
714	14	2.8	4768	4	US-09-526-193A-16	Sequence 16, Appl	c 787	14	2.8	19513	1	US-10-204-708-40	Sequence 40, Appl
715	14	2.8	4849	4	US-09-620-312D-39	Sequence 39, Appl	c 788	14	2.8	20303	1	US-08-370-975B-6	Sequence 6, Appli
716	14	2.8	4898	4	US-09-636-499-17	Sequence 17, Appl	789	14	2.8	21410	4	US-09-596-002-12	Sequence 12, Appl
717	14	2.8	5028	4	US-09-540-236-74	Sequence 74, Appl	790	14	2.8	26664	4	US-09-564-805-28	Sequence 28, Appl
718	14	2.8	5095	1	US-08-092-817-3	Sequence 3, Appli	c 791	14	2.8	26700	1	US-08-472-217-1	Sequence 1, Appli
719	14	2.8	5095	4	US-08-485-128-3	Sequence 3, Appli	c 792	14	2.8	26700	2	US-08-488-199-5	Sequence 5, Appli
720	14	2.8	5099	4	US-09-610-040-5	Sequence 5, Appli	c 793	14	2.8	26700	4	US-08-760-534A-1	Sequence 1, Appli
721	14	2.8	5176	1	US-08-447-411-1	Sequence 1, Appli	c 794	14	2.8	26700	4	US-09-336-757-1	Sequence 1, Appli
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723	14	2.8	5232	3	US-08-800-929A-3	Sequence 3, Appli	c 796	14	2.8	31063	4	US-09-596-002-20	Sequence 20, Appl
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727	14	2.8	5455	4	US-09-489-039A-4209	Sequence 4209, Ap	c 800	14	2.8	34794	4	US-09-713-678-39	Sequence 39, Appl
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C 879	13	2.6	50	4	US-08-956-171E-1905	Sequence 1905, Ap	952	13	2.6	249	4	US-09-252-991A-3017	Sequence 3017, Ap
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C 883	13	2.6	51	2	US-08-894-526-42	Sequence 42, Appl	956	13	2.6	251	4	US-09-685-166A-348	Sequence 348, App
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C 980 13 2.6 279 4 US-09-313-294A-4907 Sequence 4907, Ap
C 981 13 2.6 280 1 US-08-242-035A-3 Sequence 3, Appl
C 982 13 2.6 282 4 US-09-313-294A-5451 Sequence 5451, Ap
C 983 13 2.6 282 4 US-09-313-294A-5451 Sequence 5451, Ap
C 984 13 2.6 282 4 US-09-621-976-10843 Sequence 10843, A
C 985 13 2.6 286 4 US-09-313-294A-6296 Sequence 6296, Ap
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C 992 13 2.6 294 3 US-09-003-708A-3 Sequence 3, Appl
C 993 13 2.6 294 3 US-09-383-212-3 Sequence 3, Appl
C 994 13 2.6 294 4 US-09-489-039A-2365 Sequence 2365, Ap
C 995 13 2.6 294 4 US-09-621-976-15168 Sequence 15168, A
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C 999 13 2.6 300 4 US-09-313-294A-7176 Sequence 7176, Ap
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ALIGNMENTS

RESULT 1
US-08-866-340-12/c
; Sequence 12, Application US/08866340
; Patent No. 6020318
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
; SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,340
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keown, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-866-340-12

Query Match 3.4%; Score 17; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 177 CATAGATTGGTTTGGCT 161

RESULT 2

US-09-103-875-16/c
; Sequence 16, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-103-875-16

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Best Local Similarity 100.0%; Pred. No. 25;
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Db 1099 CATAGATTGGTTTGGCT 1083

RESULT 3

US-09-023-655-407
; Sequence 407, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

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;
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1813 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LMODNOT03
; CLONE: 1574617
US-09-023-655-407

Query Match 3.4%; Score 17; DB 4; Length 1813;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GCGAGTGGTGGCGAGG 203
DB 289 GCGAGTGGTGGCGAGG 305

RESULT 4
US-09-976-594-941/c
; Sequence 941, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 941
; LENGTH: 7055
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 346716.17
US-09-976-594-941

Query Match 3.4%; Score 17; DB 4; Length 7055;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 CCGAACCAAGCTCTGCA 165
DB 2905 CCGAACCAAGCTCTGCA 2889

RESULT 5
US-08-961-527-49
; Sequence 49, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
```

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;
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-49

Query Match 3.4%; Score 17; DB 4; Length 11443;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 327 CTCGATTTCACATGTGA 343
DB 7880 CTCGATTTCACATGTGA 7896

RESULT 6
US-08-961-527-83/c
; Sequence 83, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
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; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28473 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-83

Query Match 3.4%; Score 17; DB 4; Length 28473;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAATAAATA 360
DB 9319 TTTTTCACAAATAAATA 9303

RESULT 7
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751.389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match 3.4%; Score 17; DB 4; Length 786431;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 332 TTTTCAATGCTATTTT 348
DB 159385 TTTTCAATGCTATTTT 159401

RESULT 8
US-09-621-976-13504/c
; Sequence 13504, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13504
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13504

Query Match 3.2%; Score 16; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 85;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 189 GAGTGGGTGGCAGGT 204
DB 55 GAGTGGGTGGCAGGT 40

RESULT 9
US-09-252-991A-4718/c
; Sequence 4718, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4718
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4718

Query Match 3.2%; Score 16; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ACCTGCGCGCGAGGG 184
DB 174 ACCTGCGCGCGAGGG 159

RESULT 10
US-09-621-976-2247
; Sequence 2247, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2247
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 125..337
US-09-621-976-2247

Query Match 3.2%; Score 16; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 446 TTCTGAGCTGCTTTGT 461
DB 181 TTCTGAGCTGCTTTGT 196

RESULT 11
US-09-252-991A-4793
; Sequence 4793, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4793
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-4793

Query Match 3.2%; Score 16; DB 4; Length 612;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 ACCTGCGCGCCGAGGG 184
|||||
Db 421 ACCTGCGCGCCGAGGG 436

RESULT 12
US-09-252-991A-14857/c
; Sequence 14857, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14857
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-14857

Query Match 3.2%; Score 16; DB 4; Length 657;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 TCCGGGCGACAGCTCT 437
|||||
Db 600 TCCGGGCGACAGCTCT 585

RESULT 13
US-08-969-644-15
; Sequence 15, Application US/08969644
; Patent No. 6096519
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: pCtD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 N. Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,644
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/467,152
; FILING DATE:
; APPLICATION NUMBER: US/07/661,820
; FILING DATE:
; APPLICATION NUMBER: IT MI 91A000314
; FILING DATE: 07-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1267-202P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia trachomatis
; STRAIN: GO/86 serotype D (trachoma biovar)
; IMMEDIATE SOURCE:
; CLONE: pUC8-pGO plasmid, ATCC 68314
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..795
; US-08-969-644-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAT 359
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Db 617 TTTTTCACAAAAT 632

RESULT 14
US-08-444-189-15
; Sequence 15, Application US/08444189
; Patent No. 6110705
; GENERAL INFORMATION:
; APPLICANT: Ratti, Giulio
; APPLICANT: Comanducci, Maurizio
; APPLICANT: Tecce, Mario F.
; APPLICANT: Giuliani, Marzia M.
; TITLE OF INVENTION: pCtD PLASMID ISOLATED FROM CHLAMYDIA
; TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
; TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
; TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/180,528
FILING DATE:
APPLICATION NUMBER: US/07/991,512
FILING DATE:
APPLICATION NUMBER: US/07/661,820
FILING DATE:
APPLICATION NUMBER: IT MI 91A000314
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Chlamydia trachomatis
STRAIN: GO/86 serotype D (trachoma biovar)
IMMEDIATE SOURCE:
CLONE: pUC8-pGO plasmid, ATCC 68314
FEATURE:
NAME/KEY: CDS
LOCATION: 1..795
US-08-444-189-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAAT 359
|||||
Db 617 TTTTTCACAAAAAT 632

RESULT 15

US-08-468-544-15
Sequence 15, Application US/08468544
Patent No. 6248563

GENERAL INFORMATION:

APPLICANT: Ratti, Giulio
APPLICANT: Comanducci, Maurizio
APPLICANT: Tecce, Mario P.
APPLICANT: Giuliani, Marzia M.

TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA

TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH

STREET: 301 N. Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267-202P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Chlamydia trachomatis
STRAIN: GO/86 serotype D (trachoma biovar)
IMMEDIATE SOURCE:
CLONE: pUC8-pGO plasmid, ATCC 68314
FEATURE:
NAME/KEY: CDS
LOCATION: 1..795
US-08-468-544-15

Query Match 3.2%; Score 16; DB 3; Length 795;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 TTTTTCACAAAAAT 359
|||||
Db 617 TTTTTCACAAAAAT 632

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Job time : 101 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)

Title: US-09-987-763-7

perfect score: 500

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Database : Published Applications NA:*

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14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	134	26.8	1776	9	US-09-738-626-3211	Sequence 3211, Ap	
4	20	4.0	2550	13	US-10-424-599-127200	Sequence 127200, A	
5	19	3.8	497	10	US-09-918-595-27000	Sequence 27000, A	
6	19	3.8	15373	15	US-10-311-455-440	Sequence 440, App	
7	18	3.6	487	10	US-09-770-961-763	Sequence 763, App	
8	18	3.6	512	17	US-10-021-323-16510	Sequence 16510, A	
9	18	3.6	525	17	US-10-021-323-13895	Sequence 13895, A	
10	18	3.6	525	17	US-10-021-323-16986	Sequence 16986, A	
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12	18	3.6	557	17	US-10-021-323-12806	Sequence 12806, A	
13	18	3.6	573	17	US-10-021-323-15105	Sequence 15105, A	
14	18	3.6	578	17	US-10-021-323-13860	Sequence 13860, A	

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C 89	17	3.4	1813	17	US-10-641-643-407	Sequence 407, Appl	C 162	16	3.2	422	12	US-10-381-813-61	Sequence 61, Appl
C 90	17	3.4	1920	13	US-10-424-598-89574	Sequence 89574, A	C 163	16	3.2	429	9	US-09-960-352-10071	Sequence 10071, A
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C 92	17	3.4	2613	17	US-10-437-963-70021	Sequence 70021, A	C 165	16	3.2	430	13	US-10-424-599-29083	Sequence 29083, A
C 93	17	3.4	2617	13	US-10-425-114-35640	Sequence 35640, A	C 166	16	3.2	441	13	US-10-424-598-11125	Sequence 11125, A
C 94	17	3.4	2825	13	US-10-425-114-25100	Sequence 25100, A	C 167	16	3.2	455	11	US-09-864-408A-2861	Sequence 2861, Ap
C 95	17	3.4	3109	16	US-10-108-260A-921	Sequence 921, Appl	C 168	16	3.2	473	13	US-10-027-632-37289	Sequence 37289, A
C 96	17	3.4	3124	16	US-10-320-797-57	Sequence 57, Appl	C 169	16	3.2	476	17	US-10-027-632-37289	Sequence 37289, A
C 97	17	3.4	3335	17	US-10-437-963-70024	Sequence 70024, A	C 170	16	3.2	476	17	US-10-027-632-37289	Sequence 37289, A
C 98	17	3.4	3729	13	US-10-282-122A-37511	Sequence 37511, A	C 171	16	3.2	476	17	US-10-027-632-37289	Sequence 37289, A
C 99	17	3.4	4227	17	US-10-437-963-70015	Sequence 70015, A	C 172	16	3.2	486	9	US-10-424-598-85792	Sequence 85792, A
C 100	17	3.4	5434	9	US-09-962-436-285	Sequence 285, Appl	C 173	16	3.2	486	9	US-10-424-598-85792	Sequence 85792, A
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C 104	17	3.4	5771	15	US-10-311-455-1924	Sequence 1924, Ap	C 177	16	3.2	508	13	US-10-027-632-63686	Sequence 63686, A
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C 109	17	3.4	19553	15	US-10-092-154-1425	Sequence 1425, Ap	C 182	16	3.2	534	13	US-10-424-599-30524	Sequence 30524, A
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C 113	17	3.4	96595	12	US-10-052-482-232	Sequence 232, Appl	C 186	16	3.2	565	13	US-10-027-632-133504	Sequence 133504, A
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C 116	17	3.4	256493	13	US-10-717-597-322	Sequence 322, Appl	C 189	16	3.2	581	17	US-10-437-963-54378	Sequence 54378, A
C 117	17	3.4	439892	13	US-10-087-192-1000	Sequence 1000, Ap	C 190	16	3.2	590	13	US-10-425-114-36095	Sequence 36095, A
C 118	17	3.4	439892	13	US-10-087-192-454	Sequence 454, Appl	C 191	16	3.2	592	13	US-10-027-632-63756	Sequence 63756, A
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C 125	16	3.2	227	9	US-09-974-300-6732	Sequence 6732, Ap	C 198	16	3.2	598	13	US-10-027-632-279787	Sequence 279787, A
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C 133	16	3.2	246	13	US-10-282-122A-3940	Sequence 3940, Ap	C 206	16	3.2	606	16	US-10-027-632-48537	Sequence 48537, A
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C 136	16	3.2	246	13	US-10-282-122A-4054	Sequence 4054, Ap	C 209	16	3.2	621	17	US-10-021-323-1297	Sequence 1297, Ap
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C 143	16	3.2	274	9	US-09-783-590-2191	Sequence 2191, Ap	C 216	16	3.2	637	13	US-10-027-632-211687	Sequence 211687, A
C 144	16	3.2	303	13	US-10-282-122A-27339	Sequence 27339, A	C 217	16	3.2	637	16	US-10-027-632-211687	Sequence 211687, A
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C 146	16	3.2	327	9	US-09-983-965-3911	Sequence 3911, Appl	C 219	16	3.2	637	16	US-10-027-632-211687	Sequence 211687, A
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C 152	16	3.2	408	13	US-10-085-783A-43172	Sequence 43172, A	C 225	16	3.2	650	16	US-10-027-632-200912	Sequence 200912, A
C 153	16	3.2	411	13	US-10-242-535A-43172	Sequence 43172, A	C 226	16	3.2	651	13	US-10-027-632-200913	Sequence 200913, A
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RESULT 2
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIRO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match 55.0%; Score 275; DB 9; Length 3309400;
Best Local Similarity 99.2%; Pred. No. 1.7e-142;
Matches 475; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 3113869 GTAACCCACACCGTTTCCGCAACATGACGGGAGAGAGCCACCACTTTCGATTTC 3113810

ALIGNMENTS

RESULT 1
US-09-987-763-7
; Sequence 7, Application US/09987763
; Publication No. US20030017553A1
; GENERAL INFORMATION:
; APPLICANT: Rayapati, P. John
; APPLICANT: Crafton, Corey M.
; TITLE OF INVENTION: Nucleotide Sequences for Transcriptional Regulation in
; TITLE OF INVENTION: Corynebacterium glutamicum
; FILE REFERENCE: 1533.1940002
; CURRENT APPLICATION NUMBER: US/09/987, 763
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/248,219
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-987-763-7

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QY 262 AGCGAAACCATATTTAGTGCATCTTGCAGAGCATGACATTTCTGAGGGCATAGATTGG 321
Db 3113629 AGCGAAACCATATTTAGTGCATCTTGCAGAGCATGACATTTCTGAGGGCATAGATTGG 3113570
QY 322 TTTTGTCTGATTTACATGATTTTTCACAAATAATACATCTGCTGACCCATTT 381
Db 3113569 TTTTGTCTGATTTACATGATTTTTCACAAATAATACATCTGCTGACCCATTT 3113510
QY 382 TCGGACATATCGGCGATATTAAGGTGTAAAGGTTAACAAGGATCGGCGACAAGCTCTTGCT 441
Db 3113509 TCGGACATATCGGCGATATTAAGGTGTAAAGGTTAACAAGGATCGGCGACAAGCTCTTGCT 3113450
QY 442 GATTTTCTGAGCTGCTTTGCGGTTGCTCGGTTAGGAAATCAGGAAGTGGATCGAAA 500
Db 3113449 GATTTTCTGAGCTGCTTTGCGGTTGCTCGGTTAGGAAATCAGGAAGTGGATCGAAA 3113391

RESULT 3

US-09-738-626-3211/c
; Sequence 3211, Application US/09738626
; Publication No. US20020197605A1

GENERAL INFORMATION:

; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOHO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 3211
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-3211

Query Match 26.8%; Score 134; DB 9; Length 1776;
Best Local Similarity 100.0%; Pred. No. 6.3e-64;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GTAACCCACACCGTTTCGGCAACAATGACGGCAGAGAGCCACCATTCGCAATTTC 81
Db 251 GTAACCCACACCGTTTCGGCAACAATGACGGCAGAGAGCCACCATTCGCAATTTC 192
QY 82 GCTCCGATAAAGCCAGGCCCATATTTTCAGGAGGAGATTGCGCTGCGTTTGGCGACATT 141
Db 191 GCTCCGATAAAGCCAGGCCCATATTTTCAGGAGGAGATTGCGCTGCGTTTGGCGACATT 132

QY 142 CGGATCCCCGGAAC 155
Db 131 CGGATCCCCGGAAC 118

RESULT 4

US-10-424-599-127200/c
; Sequence 127200, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127200
; LENGTH: 2550
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85868C.1
US-10-424-599-127200

Query Match

Best Local Similarity 4.0%; Score 20; DB 13; Length 2550;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCAACAAAAATAACACTTGG 368
Db 1526 TCAACAAAAATAACACTTGG 1507

RESULT 5

US-09-918-995-27000/c
; Sequence 27000, Application US/09918995
; Publication No. US20030073623A1

GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27000
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(497)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27000

Query Match

Best Local Similarity 3.8%; Score 19; DB 10; Length 497;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AGGGAATCAGGAAGTGG 493
Db 96 AGGGAATCAGGAAGTGG 78

RESULT 6

```

US-10-311-455-440/c
; Sequence 440, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 440
; LENGTH: 15373
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;
US-10-311-455-440
Query Match 3.8%; Score 19; DB 15; Length 15373;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 TTTTTCACACAAAATAAC 362
Db 2883 TTTTTCACACAAAATAAC 2865

RESULT 7
US-09-770-961-763
; Sequence 763, Application US/09770961
; Publication No. US20030115639A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurlban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2026 (PAPA-015PRV)
; CURRENT APPLICATION NUMBER: US/09/770,961
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,466
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

```

```

US-09-770-961-763
Query Match 3.6%; Score 18; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 430 CAAGCTCTTGCTGATTTT 447
Db 467 CAAGCTCTTGCTGATTTT 484

RESULT 8
US-10-021-323-16510/c
; Sequence 16510, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16510
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-020-Q6-N6-D3
;
US-10-021-323-16510
Query Match 3.6%; Score 18; DB 17; Length 512;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 473 TTAGGAAATCAGGAAGT 490
Db 388 TTAGGAAATCAGGAAGT 371

RESULT 9
US-10-021-323-12895/c
; Sequence 12895, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12895
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-N6-E3
;
US-10-021-323-12895
Query Match 3.6%; Score 18; DB 17; Length 525;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY 473 TTAGGAAATCAGGAAGT 490
|||||
Db 421 TTAGGAAATCAGGAAGT 404

RESULT 10

US-10-021-323-16986/c
; Sequence 16986, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16986
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; LOCATION: (1)..(557)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-026-Q6-N6-E2
US-10-021-323-16986

Query Match 3.6%; Score 18; DB 17; Length 525;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGAAATCAGGAAGT 490
|||||
Db 430 TTAGGAAATCAGGAAGT 413

RESULT 11

US-10-021-323-16193/c
; Sequence 16193, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 16193
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-015-Q1-N6-G5
US-10-021-323-16193

Query Match 3.6%; Score 18; DB 17; Length 544;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGAAATCAGGAAGT 490
|||||
Db 406 TTAGGAAATCAGGAAGT 389

RESULT 12

US-10-021-323-12806
; Sequence 12806, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 12806
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(557)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-007-Q6-K6-E3
US-10-021-323-12806

Query Match 3.6%; Score 18; DB 17; Length 557;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGAAATCAGGAAGT 490
|||||
Db 132 TTAGGAAATCAGGAAGT 149

RESULT 13

US-10-021-323-15105
; Sequence 15105, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 15105
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-020-Q6-K6-D3
US-10-021-323-15105

Query Match 3.6%; Score 18; DB 17; Length 573;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGAAATCAGGAAGT 490
|||||
Db 207 TTAGGAAATCAGGAAGT 224

RESULT 14

Fri Aug 6 10:32:27 2004

US-10-021-323-13860
; Sequence 13860, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 13860
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(578)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3829-015-Q1-K6-G5
US-10-021-323-13860

Query Match 3.6%; Score 18; DB 17; Length 578;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 TTAGGGAATCAGGAAGT 490
Db 197 TTAGGGAATCAGGAAGT 214

RESULT 15
US-09-918-995-12576/c
; Sequence 12576, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12576
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(584)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-12576

Query Match 3.6%; Score 18; DB 10; Length 584;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 TTCTGCAGGCATAGATT 319
Db 475 TTCTGCAGGCATAGATT 458

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2004, 14:18:07 ; Search time 2385 Seconds
(without alignments)

6260.415 Million cell updates/sec

Title: US-09-987-763-7

Perfect score: 500

Sequence: 1 aaacagccaggttagcggc.....atcagggaagtggaatcgaaa 500

Scoring table: OLIGO NUC

Gapop_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST:*

1: em_estba:**

2: em_esthum:**

3: em_estin:**

4: em_estnu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_htc:**

9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pin:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	4.2	801	29	CC529519 CH240 405
2	21	4.2	973	13	BU519692 AGENCOURT
3	20	4.0	213	29	CE545692 tigr-gss-
4	20	4.0	346	28	AQ959051 LEREG96TR

C	5	20	4.0	360	14	CA912211	PCS02658
C	6	20	4.0	393	12	BM892066	Sam47H05.
C	7	20	4.0	490	9	AU203244	AU203244
	8	20	4.0	539	9	AV960301	AV960301
C	9	20	4.0	541	13	BM204471	BM204471
C	10	20	4.0	551	13	BM521341	BM521341
C	11	20	4.0	557	12	BI944599	BI944599
C	12	20	4.0	570	13	BM277800	BM277800
C	13	20	4.0	574	13	BQ296476	BQ296476
C	14	20	4.0	577	12	BI943495	BI943495
C	15	20	4.0	581	28	AZ493804	AZ493804
C	16	20	4.0	587	10	BE805810	BE805810
C	17	20	4.0	590	10	AW759418	AW759418
C	18	20	4.0	614	12	BJ110320	BJ110320
C	19	20	4.0	616	12	BJ110370	BJ110370
C	20	20	4.0	617	10	AW279214	AW279214
C	21	20	4.0	621	9	AU207364	AU207364
C	22	20	4.0	633	28	AZ869794	AZ869794
C	23	20	4.0	655	13	BM216978	BM216978
C	24	20	4.0	673	14	CF243553	CF243553
C	25	20	4.0	689	14	CF806395	CF806395
C	26	20	4.0	698	13	BM214172	BM214172
C	27	20	4.0	727	12	BP014381	BP014381
C	28	20	4.0	788	28	BH729346	BH729346
C	29	20	4.0	843	14	CK250567	CK250567
C	30	20	4.0	915	14	CK258134	CK258134
C	31	20	4.0	920	14	CK254139	CK254139
C	32	20	4.0	922	14	CK258904	CK258904
C	33	20	4.0	945	28	AZ166685	AZ166685
C	34	20	4.0	974	14	CK251495	CK251495
C	35	20	4.0	978	14	CK254992	CK254992
C	36	20	4.0	1006	14	CK250376	CK250376
C	37	20	4.0	1167	28	CC268378	CC268378
C	38	19	3.8	343	14	CD673749	CD673749
C	39	19	3.8	386	14	R73793	R73793
C	40	19	3.8	430	14	H29150	H29150
C	41	19	3.8	447	14	T09037	T09037
C	42	19	3.8	454	10	BF713406	BF713406
C	43	19	3.8	461	14	CB736812	CB736812
C	44	19	3.8	482	9	AU231249	AU231249
C	45	19	3.8	515	13	BQ856912	BQ856912
C	46	19	3.8	521	10	BE252127	BE252127
C	47	19	3.8	521	28	BZ675425	BZ675425
C	48	19	3.8	549	29	CE284696	CE284696
C	49	19	3.8	559	28	BH044780	BH044780
C	50	19	3.8	590	12	BM722923	BM722923
C	51	19	3.8	592	12	BJ434874	BJ434874
C	52	19	3.8	620	28	AZ634145	AZ634145
C	53	19	3.8	637	29	CC749924	CC749924
C	54	19	3.8	638	12	BM706879	BM706879
C	55	19	3.8	640	29	CE257551	CE257551
C	56	19	3.8	649	13	BQ578571	BQ578571
C	57	19	3.8	653	10	BE255492	BE255492
C	58	19	3.8	676	9	AI584574	AI584574
C	59	19	3.8	689	10	BB375011	BB375011
C	60	19	3.8	717	28	BZ415107	BZ415107
C	61	19	3.8	756	9	AI721333	AI721333
C	62	19	3.8	759	29	CE079578	CE079578
C	63	19	3.8	768	12	BG110902	BG110902
C	64	19	3.8	789	28	BZ419232	BZ419232
C	65	19	3.8	828	28	BH430252	BH430252
C	66	19	3.8	829	28	BH706484	BH706484
C	67	19	3.8	830	28	BZ638567	BZ638567
C	68	19	3.8	859	28	BH422618	BH422618
C	69	19	3.8	862	28	BZ788270	BZ788270
C	70	19	3.8	862	29	CG049916	CG049916
C	71	19	3.8	876	12	BG192528	BG192528
C	72	19	3.8	877	29	CG971007	CG971007
C	73	19	3.8	880	28	CC404611	CC404611
C	74	19	3.8	893	29	CG127404	CG127404
C	75	19	3.8	899	13	BU508902	BU508902
C	76	19	3.8	910	10	BE894163	BE894163
C	77	19	3.8	919	28	CC390023	CC390023

C 78	19	3.8	924	29	CG947826	CG947826 MBEJC65TF	151	18	3.6	638	28	AZ406401
C 79	19	3.8	934	29	CNS01KHU	AL1148355 Anopheles	C 152	18	3.6	646	29	CE841301
C 80	19	3.8	939	29	CG304202	CG304202 CGXC266TH	153	18	3.6	648	12	BJ543393
C 81	19	3.8	940	29	CG366263	CG366263 PUHNT31TD	154	18	3.6	657	13	EX301727
C 82	19	3.8	955	29	CG026168	CG026168 ZMMBC056	C 155	18	3.6	679	13	BW009367
C 83	19	3.8	988	12	BM474134	BM474134 AGENCOURT	C 156	18	3.6	681	13	BO402195
C 84	19	3.8	1233	12	BM546655	BM546655 AGENCOURT	C 157	18	3.6	687	14	CF325795
C 85	19	3.8	2057	11	AK081795	AK081795 Mus muscu	C 158	18	3.6	689	28	BF999275
C 86	18	3.6	112	12	BJ365130	BJ365130 BJ365130	C 159	18	3.6	692	13	CA063584
C 87	18	3.6	115	12	BJ365299	BJ365299 BJ365299	C 160	18	3.6	695	12	BI548831
C 88	18	3.6	129	12	BJ370960	BJ370960 BJ370960	C 161	18	3.6	699	13	BY709232
C 89	18	3.6	133	12	BJ392064	BJ392064 BJ392064	C 162	18	3.6	706	28	BH842871
C 90	18	3.6	142	12	BP522231	BP522231 BP522231	163	18	3.6	710	29	AG101703
C 91	18	3.6	150	12	BJ396709	BJ396709 BJ396709	164	18	3.6	715	28	BH950483
C 92	18	3.6	204	28	BZ149860	BZ149860 CH230-359	165	18	3.6	719	13	BY764464
C 93	18	3.6	205	13	EX680967	EX680967 EX680967	C 166	18	3.6	722	14	CK247466
C 94	18	3.6	242	9	AV341489	AV341489 AV341489	C 167	18	3.6	728	10	BE292438
C 95	18	3.6	266	28	BI741865	BI741865 kt61h12.Y	C 168	18	3.6	731	28	BH968929
C 96	18	3.6	274	10	BA496689	BA496689 BA496689	C 169	18	3.6	737	28	BH794283
C 97	18	3.6	286	10	BF713653	BF713653 ESTPBL200	C 170	18	3.6	742	12	BI757516
C 98	18	3.6	298	10	BE103413	BE103413 UI-R-BX0-	C 171	18	3.6	749	29	CE838709
C 99	18	3.6	319	29	CG798404	CG798404 SALK 1462	C 172	18	3.6	758	29	EX211946
C 100	18	3.6	335	9	AI396114	AI396114 487011F09	C 173	18	3.6	766	28	BH211256
C 101	18	3.6	335	12	BI741865	BI741865 kt61h12.Y	C 174	18	3.6	768	13	BU707899
C 102	18	3.6	363	9	AA825471	AA825471 od04b04.s	C 175	18	3.6	773	13	BI199494
C 103	18	3.6	365	10	BE045085	BE045085 hm28c02.x	C 176	18	3.6	778	12	BI422441
C 104	18	3.6	372	28	AQ045467	AQ045467 RPI111-36	C 177	18	3.6	791	12	CG109823
C 105	18	3.6	379	13	EX502009	EX502009 DKFZP779F	C 178	18	3.6	794	12	BI549285
C 106	18	3.6	395	12	BG301443	BG301443 kt01c01.Y	C 179	18	3.6	795	29	CC487994
C 107	18	3.6	396	12	BG301652	BG301652 kt03g09.Y	C 180	18	3.6	802	28	BZ401265
C 108	18	3.6	411	9	AI549192	AI549192 UI-R-C3-t	C 181	18	3.6	803	12	BI912821
C 109	18	3.6	414	9	AI825477	AI825477 wb73d06.x	C 182	18	3.6	808	12	EG445766
C 110	18	3.6	431	29	CC860561	CC860561 NDL.26M6.	C 183	18	3.6	810	12	EG114422
C 111	18	3.6	458	10	BF224006	BF224006 7g36f06.x	C 184	18	3.6	815	28	BH645807
C 112	18	3.6	472	28	BH844363	BH844363 TC3-55J14	C 185	18	3.6	820	28	CC067387
C 113	18	3.6	473	12	BG347817	BG347817 dae80d12.x	C 186	18	3.6	828	28	EX213922
C 114	18	3.6	493	10	BF059589	BF059589 7k63b12.x	C 187	18	3.6	831	28	BZ389182
C 115	18	3.6	493	28	AZ924819	AZ924819 4906.1d55	C 188	18	3.6	831	28	BZ399886
C 116	18	3.6	505	14	CD542221	CD542221 B0238E12-	C 189	18	3.6	831	29	CG112105
C 117	18	3.6	526	14	CD542568	CD542568 B0242A02-	C 190	18	3.6	840	28	BZ393980
C 118	18	3.6	530	12	BX301726	BX301726 BX301726	C 191	18	3.6	850	28	AZ674369
C 119	18	3.6	531	12	BP522327	BP522327 BP522327	C 192	18	3.6	852	13	BQ509370
C 120	18	3.6	541	10	BF266205	BF266205 HV_CEA001	C 193	18	3.6	860	12	BI768310
C 121	18	3.6	544	28	BH195592	BH195592 TC3-4E9.T	C 194	18	3.6	862	12	EG447093
C 122	18	3.6	551	14	CD525790	CD525790 kw26a10.Y	C 195	18	3.6	873	28	BH155174
C 123	18	3.6	562	9	AV553806	AV553806 AV553806	C 196	18	3.6	874	10	BF279440
C 124	18	3.6	565	14	CF202319	CF202319 RR890915N	C 197	18	3.6	875	14	CK252826
C 125	18	3.6	568	13	BQ738972	BQ738972 PC38g12.Y	C 198	18	3.6	879	29	CG762526
C 126	18	3.6	570	13	BQ692111	BQ692111 pt03a08.Y	C 199	18	3.6	886	13	BU956652
C 127	18	3.6	573	10	BQ053511	BQ053511 GA_Ea002	C 200	18	3.6	889	28	AZ674182
C 128	18	3.6	573	13	BQ408123	BQ408123 GA_Ed000	C 201	18	3.6	892	29	CG976368
C 129	18	3.6	573	13	BQ408124	BQ408124 GA_Ed000	C 202	18	3.6	894	28	CG976368
C 130	18	3.6	575	9	AU236000	AU236000 AU236000	C 203	18	3.6	894	28	CG976368
C 131	18	3.6	575	10	AW616607	AW616607 EST223018	C 204	18	3.6	900	13	BX342290
C 132	18	3.6	577	28	AQ518331	AQ518331 HS_5102.B	C 205	18	3.6	904	13	BU159221
C 133	18	3.6	594	10	BE055030	BE055030 GA_Ea001	C 206	18	3.6	918	28	CC078983
C 134	18	3.6	595	13	BQ405675	BQ405675 GA_Ed008	C 207	18	3.6	925	13	BQ223735
C 135	18	3.6	595	14	CF107618	CF107618 Shultztzmi	C 208	18	3.6	927	29	CG650230
C 136	18	3.6	597	12	BQ445288	BQ445288 GA_Ea002	C 209	18	3.6	927	29	CG650230
C 137	18	3.6	600	13	BQ603343	BQ603343 MI-P-NA-a	C 210	18	3.6	932	28	BZ680565
C 138	18	3.6	606	29	CE574126	CE574126 tigr-988-	C 211	18	3.6	948	10	BF168433
C 139	18	3.6	607	13	BQ415092	BQ415092 GA_Ed009	C 212	18	3.6	984	28	CC299564
C 140	18	3.6	611	28	BZ393490	BZ393490 EINBB65TF	C 213	18	3.6	986	12	BG334996
C 141	18	3.6	613	28	AQ262931	AQ262931 CITBI-EI-	C 214	18	3.6	995	29	CG650238
C 142	18	3.6	622	12	BM988514	BM988514 UI-H-DHO-	C 215	18	3.6	999	10	BE454301
C 143	18	3.6	622	29	CE028049	CE028049 tigr-988-	C 216	18	3.6	1005	12	BM454001
C 144	18	3.6	624	13	CD486484	CD486484 CRH3.ID11	C 217	18	3.6	1012	12	BI488630
C 145	18	3.6	628	13	BQ402196	BQ402196 GA_Ed004	C 218	18	3.6	1071	10	BF964867
C 146	18	3.6	628	13	CD486484	CD486484 CRH3.ID11	C 219	18	3.6	1100	29	CNS04255
C 147	18	3.6	630	13	BQ413831	BQ413831 BOMEL51TF	C 220	18	3.6	1120	28	CC292953
C 148	18	3.6	631	13	BX680735	BX680735 BX680735	C 221	18	3.6	1120	28	CC292953
C 149	18	3.6	633	14	CD813917	CD813917 EN15.02IG	C 222	18	3.6	1479	28	CC324015
C 150	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 223	18	3.6	2687	11	BC042192
C 151	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 224	18	3.6	2687	11	BC042192
C 152	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 225	18	3.6	2687	11	BC042192
C 153	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 226	18	3.6	2687	11	BC042192
C 154	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 227	18	3.6	2687	11	BC042192
C 155	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 228	18	3.6	2687	11	BC042192
C 156	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 229	18	3.6	2687	11	BC042192
C 157	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 230	18	3.6	2687	11	BC042192
C 158	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 231	18	3.6	2687	11	BC042192
C 159	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 232	18	3.6	2687	11	BC042192
C 160	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 233	18	3.6	2687	11	BC042192
C 161	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 234	18	3.6	2687	11	BC042192
C 162	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 235	18	3.6	2687	11	BC042192
C 163	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 236	18	3.6	2687	11	BC042192
C 164	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 237	18	3.6	2687	11	BC042192
C 165	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 238	18	3.6	2687	11	BC042192
C 166	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 239	18	3.6	2687	11	BC042192
C 167	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 240	18	3.6	2687	11	BC042192
C 168	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 241	18	3.6	2687	11	BC042192
C 169	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 242	18	3.6	2687	11	BC042192
C 170	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 243	18	3.6	2687	11	BC042192
C 171	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 244	18	3.6	2687	11	BC042192
C 172	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 245	18	3.6	2687	11	BC042192
C 173	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 246	18	3.6	2687	11	BC042192
C 174	18	3.6	634	10	BF272467	BF272467 GA_EB001	C 247	18	3.6	2687	11	BC042192
C 175	18	3.6	634	10								

C 224	18	3-6	2688	11	BC030284	BC030284 Homo sapi	C 297	17	3-4	382	29	CG021490
C 225	18	3-6	3396	11	AK089442	AK089442 Mus muscu	C 298	17	3-4	383	12	BG900748
C 226	17	3-4	56	29	BX209742	BX209742 Danio rer	C 299	17	3-4	383	13	BY372025
C 227	17	3-4	94	9	AA503707	AA503707 ns50d12.s	C 300	17	3-4	387	11	CNS093RS
C 228	17	3-4	146	9	AI006254	AI006254 ua88g04.f	C 301	17	3-4	389	12	BJ140510
C 229	17	3-4	197	12	BI007827	BI007827 QV3-RTO07	C 302	17	3-4	389	12	BJ183744
C 230	17	3-4	204	13	BW170281	BW170281 BW170281	C 303	17	3-4	392	9	AA197676
C 231	17	3-4	204	28	AQ974424	AQ974424 RPT-23-3	C 304	17	3-4	396	28	AA197676
C 232	17	3-4	218	29	CE498075	CE498075 tigr-gss-	C 305	17	3-4	396	28	AA197676
C 233	17	3-4	221	29	BX204239	BX204239 Danio rer	C 306	17	3-4	396	28	AA197676
C 234	17	3-4	236	10	BB301122	BB301122 BB301122	C 307	17	3-4	396	28	AA197676
C 235	17	3-4	236	28	AZ379779	AZ379779 IM013511	C 308	17	3-4	399	9	AA139630
C 236	17	3-4	239	12	BM418295	BM418295 952013H01	C 309	17	3-4	407	29	AG029027
C 237	17	3-4	240	10	BB170277	BB170277 BB170277	C 310	17	3-4	409	28	BJ200918
C 238	17	3-4	240	13	C31037	C31037 C31037 Yyji	C 311	17	3-4	409	28	BJ200918
C 239	17	3-4	240	13	C58876	C58876 C58876 Yyji	C 312	17	3-4	410	10	BE247755
C 240	17	3-4	244	14	H34292	H34292 EST11070.R	C 313	17	3-4	410	10	BE247755
C 241	17	3-4	248	13	BR300139	BR300139 BR300139	C 314	17	3-4	412	13	B0430303
C 242	17	3-4	255	14	W89747	W89747 mf75d03.r1	C 315	17	3-4	413	28	AQ528831
C 243	17	3-4	264	10	BE022146	BE022146 sm68a10.Y	C 316	17	3-4	417	29	BX197777
C 244	17	3-4	267	10	BB372134	BB372134 BB372134	C 317	17	3-4	420	13	BX480118
C 245	17	3-4	268	9	AV134545	AV134545 AV134545	C 318	17	3-4	421	28	CC160358
C 246	17	3-4	268	14	CB945859	CB945859 AGENCOURT	C 319	17	3-4	421	28	CC160358
C 247	17	3-4	271	10	BB576952	BB576952 BB576952	C 320	17	3-4	421	28	CC160358
C 248	17	3-4	275	10	BB195768	BB195768 BB195768	C 321	17	3-4	425	10	AW894114
C 249	17	3-4	278	10	BB552429	BB552429 BB552429	C 322	17	3-4	425	28	AZ919276
C 250	17	3-4	279	10	BB455278	BB455278 BB455278	C 323	17	3-4	430	10	BF990273
C 251	17	3-4	284	28	BZ956930	BZ956930 PGH005E10	C 324	17	3-4	430	29	CC870478
C 252	17	3-4	287	10	BB400137	BB400137 BB400137	C 325	17	3-4	433	9	AA000841
C 253	17	3-4	289	10	BB022169	BB022169 BB022169	C 326	17	3-4	436	12	BG240668
C 254	17	3-4	295	10	BB547695	BB547695 BB547695	C 327	17	3-4	436	28	BH4433508
C 255	17	3-4	295	28	AZ261437	AZ261437 RPT-23-4	C 328	17	3-4	437	12	BG518032
C 256	17	3-4	298	14	D71093	D71093 CELK062A4R	C 329	17	3-4	442	13	BQ207915
C 257	17	3-4	299	10	BB179024	BB179024 BB179024	C 330	17	3-4	443	13	BQ207915
C 258	17	3-4	300	9	AV118395	AV118395 AV118395	C 331	17	3-4	443	13	BQ207915
C 259	17	3-4	300	9	AV179873	AV179873 AV179873	C 332	17	3-4	446	10	BF284630
C 260	17	3-4	300	9	AV180188	AV180188 AV180188	C 333	17	3-4	446	12	BI662660
C 261	17	3-4	300	9	AV180416	AV180416 AV180416	C 334	17	3-4	450	9	AL589262
C 262	17	3-4	300	9	AV182745	AV182745 AV182745	C 335	17	3-4	451	10	BE556224
C 263	17	3-4	300	10	BB190034	BB190034 BB190034	C 336	17	3-4	452	14	W95278
C 264	17	3-4	300	13	C31586	C31586 C31586 Yyji	C 337	17	3-4	453	12	BI425240
C 265	17	3-4	300	13	C32629	C32629 C32629 Yyji	C 338	17	3-4	454	12	BG346646
C 266	17	3-4	300	13	C33146	C33146 C33146 Yyji	C 339	17	3-4	455	13	B0815558
C 267	17	3-4	302	13	BU429125	BU429125 UI-HF-BNO	C 340	17	3-4	455	28	AQ598793
C 268	17	3-4	304	10	BB188452	BB188452 BB188452	C 341	17	3-4	458	10	BF069257
C 269	17	3-4	309	9	AA144291	AA144291 mr80c04.r	C 342	17	3-4	458	13	BY152165
C 270	17	3-4	309	9	AI822384	AI822384 I0-837T3	C 343	17	3-4	459	28	AQ523668
C 271	17	3-4	310	9	AA379007	AA379007 EST91773	C 344	17	3-4	461	28	AZ839742
C 272	17	3-4	312	28	CC045458	CC045458 3591.1.17	C 345	17	3-4	462	29	DR5B9T
C 273	17	3-4	313	10	BB266286	BB266286 BB266286	C 346	17	3-4	464	9	AA722948
C 274	17	3-4	317	13	C96591	C96591 C96591 Marc	C 347	17	3-4	466	10	AW504614
C 275	17	3-4	318	9	AA093687	AA093687 cl0573.re	C 348	17	3-4	469	9	AI172393
C 276	17	3-4	322	9	AI850687	AI850687 UI-M-BG1-	C 349	17	3-4	470	9	BE332853
C 277	17	3-4	322	9	AU710680	AU710680 AU210680	C 350	17	3-4	470	9	AI645119
C 278	17	3-4	325	9	AA769092	AA769092 ca74f03.s	C 351	17	3-4	470	9	AA497449
C 279	17	3-4	325	9	AA457593	AA457593 aa89a02.r	C 352	17	3-4	471	9	AI645840
C 280	17	3-4	328	9	AA062436	AA062436 CM0-CT004	C 353	17	3-4	473	28	BZ622502
C 281	17	3-4	334	9	AA631891	AA631891 np69c11.s	C 354	17	3-4	476	13	B0040380
C 282	17	3-4	338	9	AI299785	AI299785 gn09a12.x	C 355	17	3-4	479	29	CE032418
C 283	17	3-4	340	12	BG346574	BG346574 daa38d12.	C 356	17	3-4	480	14	CB386468
C 284	17	3-4	341	28	AQ453345	AQ453345 LMAJFV1.1	C 357	17	3-4	480	28	AQ857789
C 285	17	3-4	342	9	AI505804	AI505804 vi43a03.x	C 358	17	3-4	485	29	CE623590
C 286	17	3-4	350	9	AU044475	AU044475 AU044475	C 359	17	3-4	486	9	AI029460
C 287	17	3-4	351	13	BU020153	BU020153 QHE26J01.	C 360	17	3-4	487	12	BM276840
C 288	17	3-4	356	10	AW545012	AW545012 C0188F02-	C 361	17	3-4	487	13	BX517845
C 289	17	3-4	357	28	BH884533	BH884533 hw52e11.g	C 362	17	3-4	488	28	BZ252606
C 290	17	3-4	362	29	LEWFD15	LEWFD15 BX530447 Leishmani	C 363	17	3-4	491	9	AA144528
C 291	17	3-4	363	13	BY415455	BY415455 BY415455	C 364	17	3-4	493	14	CB642978
C 292	17	3-4	365	9	AI851326	AI851326 UI-M-BHO-	C 365	17	3-4	495	12	BM970188
C 293	17	3-4	372	28	AZ720459	AZ720459 RPT-24-1	C 366	17	3-4	496	28	AZ920560
C 294	17	3-4	377	14	H08903	H08903 Y188608.r1	C 367	17	3-4	497	11	CNS09050
C 295	17	3-4	382	10	AW503403	AW503403 UI-HF-BNO	C 368	17	3-4	502	10	BE235625
C 296	17	3-4	382	28	AZ596568	AZ596568 1M0409J22	C 369	17	3-4	502	14	CA507675

370	17	3.4	503	10	BE234827	142076 MA	443	17	3.4	611	28	BZ396350
371	17	3.4	508	28	BH205806	Sm1-59K21	444	17	3.4	612	13	BU720472
372	17	3.4	509	28	BZ366237	ic95e11.b	445	17	3.4	613	10	AW958341
373	17	3.4	511	10	BE949917	UT-M-CD0-	446	17	3.4	614	14	CB826216
374	17	3.4	512	10	BF547971	UT-R-E0-b	C 447	17	3.4	614	14	CF108178
375	17	3.4	514	28	CF547021	1157904.b	C 448	17	3.4	614	29	DR41D5T
376	17	3.4	515	13	CF631501	UT-HF-BN0	C 449	17	3.4	615	13	BU046390
377	17	3.4	516	14	CF631501	zmrw848_0	C 450	17	3.4	615	29	AG034990
378	17	3.4	519	10	BQ019901	ux04902.x	C 451	17	3.4	616	9	AL777133
379	17	3.4	523	13	BZ296182	gan87h03	C 452	17	3.4	616	14	CD995047
380	17	3.4	525	13	BX529099	EX529099	C 453	17	3.4	616	28	AQ504602
381	17	3.4	525	14	CA951631	in80c07.x	C 454	17	3.4	617	12	BQ13471
382	17	3.4	528	10	BE017207	FR77h05.y	C 455	17	3.4	617	29	CE220286
383	17	3.4	529	10	BE336122	u85e06.y	C 456	17	3.4	620	12	B1943651
384	17	3.4	529	28	AZ635626	1M0493D05	C 457	17	3.4	622	12	BM719104
385	17	3.4	531	12	BU144969	BU144969	C 458	17	3.4	622	13	BU304458
386	17	3.4	532	10	BF921494	BF921494	C 459	17	3.4	625	13	CA041174
387	17	3.4	532	10	BF346572	BF346572	C 460	17	3.4	627	29	CE413548
388	17	3.4	533	10	BF959478	BF959478	C 461	17	3.4	628	28	AZ861189
389	17	3.4	539	9	AU040106	AU040106	C 462	17	3.4	630	11	CNS09DU1
390	17	3.4	539	28	BZ677400	PUBBX30TD	C 463	17	3.4	630	13	BU720459
391	17	3.4	540	28	CE160415	ig08g11.y	C 464	17	3.4	632	13	BX265897
392	17	3.4	541	10	BG007940	QYA-GN012	C 465	17	3.4	632	14	CD074694
393	17	3.4	541	14	CD721977	OJ03h07.y	C 466	17	3.4	632	13	BU824766
394	17	3.4	543	29	CG558279	OST434146	C 467	17	3.4	633	13	BQ110879
395	17	3.4	545	14	CA892793	BU174G02-	C 468	17	3.4	636	28	BZ317309
396	17	3.4	546	10	AW500273	UT-HF-BN0	C 469	17	3.4	636	28	BZ317309
397	17	3.4	547	28	AQ793036	HS 5323_B	C 470	17	3.4	637	13	BX344665
398	17	3.4	550	9	AV719416	AV719416	C 471	17	3.4	638	13	BQ265896
399	17	3.4	552	13	BU288458	604164433	C 472	17	3.4	638	28	AQ247896
400	17	3.4	555	14	CF138280	UT-HF-BN0	C 473	17	3.4	639	10	AW551711
401	17	3.4	558	29	CE636215	tigr-gss-	C 474	17	3.4	641	12	BG573770
402	17	3.4	559	10	BE813907	QV3-BN004	C 475	17	3.4	641	13	BU287460
403	17	3.4	561	28	AQ110202	HS 5220_A	C 476	17	3.4	642	13	BU289975
404	17	3.4	564	28	BZ395340	EINAW96Tr	C 477	17	3.4	642	28	BZ415530
405	17	3.4	570	29	CE082576	CG582576	C 478	17	3.4	643	29	CG066082
406	17	3.4	570	29	CG980089	CH240_159	C 479	17	3.4	645	28	BZ339796
407	17	3.4	571	28	BH777894	BH777894	C 480	17	3.4	645	28	BZ339796
408	17	3.4	572	28	BZ817270	PUGAC05TB	C 481	17	3.4	647	28	BZ366238
409	17	3.4	574	28	BH747639	BH747639	C 482	17	3.4	648	10	AW552085
410	17	3.4	578	12	BU117304	BU117304	C 483	17	3.4	649	13	BU647740
411	17	3.4	578	12	BU117304	BU117304	C 484	17	3.4	649	13	BX698433
412	17	3.4	578	29	CE725339	CE725339	C 485	17	3.4	650	13	BQ388027
413	17	3.4	579	14	CF628962	zmrw648_0	C 486	17	3.4	651	12	BM603374
414	17	3.4	580	28	AQ463929	HS 5074_B	C 487	17	3.4	651	12	BM706900
415	17	3.4	583	9	AL723998	AL723998	C 488	17	3.4	651	12	BM706900
416	17	3.4	583	29	CE338444	tigr-gss-	C 489	17	3.4	652	13	BX483764
417	17	3.4	585	28	AZ007651	RPCI-23-3	C 490	17	3.4	652	28	BZ618788
418	17	3.4	586	28	AZ108677	AZ108677	C 491	17	3.4	652	28	BZ618788
419	17	3.4	587	13	C87034	C87034	C 492	17	3.4	654	13	BU288602
420	17	3.4	589	9	AU020974	AU020974	C 493	17	3.4	655	29	CG676339
421	17	3.4	589	28	BZ148280	BZ148280	C 494	17	3.4	657	29	BX127461
422	17	3.4	589	28	BZ775715	ib95e02.g	C 495	17	3.4	658	28	AZ131595
423	17	3.4	590	9	AU199285	AU199285	C 496	17	3.4	659	9	AJ397959
424	17	3.4	591	29	CG335420	CG335420	C 497	17	3.4	659	28	AQ163365
425	17	3.4	593	11	AK012687	Mus muscu	C 498	17	3.4	660	13	BU559373
426	17	3.4	594	14	CA365505	CA365505	C 499	17	3.4	661	10	BE309138
427	17	3.4	594	28	BH010450	ep62f11.b	C 500	17	3.4	662	14	CA510001
428	17	3.4	598	11	CNS09G00	Single re	C 501	17	3.4	664	29	CC845663
429	17	3.4	599	28	BH057836	RPCI-24-9	C 502	17	3.4	664	29	AG171490
430	17	3.4	601	9	AV006563	AV006563	C 503	17	3.4	665	11	CNS09072
431	17	3.4	601	14	CF796110	CF796110	C 504	17	3.4	665	28	CNS01069
432	17	3.4	602	10	BG067651	H3056F12-	C 505	17	3.4	669	28	BH202683
433	17	3.4	602	28	BH590137	BOHKF30TF	C 506	17	3.4	673	14	CD331479
434	17	3.4	603	13	BU041757	BU041757	C 507	17	3.4	677	28	CC169173
435	17	3.4	604	12	BZ335154	BZ335154	C 508	17	3.4	678	10	AW556398
436	17	3.4	605	12	BH101025	BH101025	C 509	17	3.4	679	12	BM641037
437	17	3.4	605	13	BU121734	BU121734	C 510	17	3.4	679	13	BU240379
438	17	3.4	605	28	BZ344565	BZ344565	C 511	17	3.4	679	28	BZ618080
439	17	3.4	608	14	CF011760	QBK12C04	C 512	17	3.4	680	28	BZ338424
440	17	3.4	609	14	CF071688	PE1_18.D0	C 513	17	3.4	681	28	AZ599672
441	17	3.4	610	11	CNS09072	Single re	C 514	17	3.4	682	11	CNS09GP2
442	17	3.4	611	13	BX261285	BX261285	C 515	17	3.4	683	28	BH884532

C 516	17	3.4	683	18	BZ622607	ig79e02.b	589	17	3.4	759	29	CG022869	CG022869	ZNMBC055
C 517	17	3.4	684	24	CB971126	CAB10004	590	17	3.4	762	13	BU287962	BU287962	604161908
C 518	17	3.4	684	28	BZ005762	oei27b05	591	17	3.4	763	13	AA877828	AA877828	nrl1h09.s
C 519	17	3.4	684	28	BZ777191	ii08c10.g	592	17	3.4	764	13	BU289555	BU289555	603605947
C 520	17	3.4	688	28	BH877568	hr39b02.b	593	17	3.4	764	13	BU232958	BU232958	603869062
C 521	17	3.4	689	12	BM609510	170006871	594	17	3.4	765	13	BU222848	BU222848	603400157
C 522	17	3.4	689	14	CF971556	AUB_1flvr	595	17	3.4	765	13	BU378499	BU378499	603590512
C 523	17	3.4	690	10	BB117845	BB117845	596	17	3.4	769	11	CNS0938D	BU689485	nhxb0079B
C 524	17	3.4	690	13	BU280891	603866970	597	17	3.4	772	28	AQ689485	AQ689485	603502088
C 525	17	3.4	691	28	AZ574149	325PVD05	598	17	3.4	773	13	BU260503	BU260503	603502088
C 526	17	3.4	693	28	BH118237	RPCT-24-2	599	17	3.4	773	28	AQ865561	AQ865561	nbeb0025H
C 527	17	3.4	694	14	CF135612	UI-HF-BN0	600	17	3.4	774	13	BU121284	BU121284	603146486
C 528	17	3.4	694	14	CF135613	UI-HF-BN0	601	17	3.4	776	13	BU122191	BU122191	603003010
C 529	17	3.4	695	28	AZ631628	IM0485H20	602	17	3.4	779	14	CB633848	CB633848	OS1fBb12P
C 530	17	3.4	695	28	BZ629698	BZ629698	603	17	3.4	780	29	CE039852	CE039852	tigr-gss-
C 531	17	3.4	697	29	CE216622	CE216622	604	17	3.4	782	13	BU120963	BU120963	603003074
C 532	17	3.4	697	29	AG135355	Pan_trogl	605	17	3.4	784	28	BZ679449	BZ679449	PUBHS207D
C 533	17	3.4	699	13	BY762721	BY762721	606	17	3.4	786	28	AZ139125	AZ139125	SP_0178.B
C 534	17	3.4	699	28	BH010577	ep66c02.b	607	17	3.4	786	28	BZ399682	BZ399682	EINCS34TR
C 535	17	3.4	700	12	BH586565	BH586565	608	17	3.4	790	28	CC422855	CC422855	PURWE14TD
C 536	17	3.4	700	13	BU374008	BU374008	609	17	3.4	791	14	CB901936	CB901936	603146486
C 537	17	3.4	700	14	CD824276	BN25_053A	610	17	3.4	791	28	CB392033	CB392033	tiic028Xg
C 538	17	3.4	703	28	BH514665	BH514665	611	17	3.4	793	28	BZ386087	BZ386087	EINAT92TR
C 539	17	3.4	703	14	CA174266	CA174266	612	17	3.4	793	28	BZ386087	BZ386087	EINAT92TR
C 540	17	3.4	703	28	BH951144	odj27f01	613	17	3.4	794	13	BZ386950	BZ386950	EINCL567F
C 541	17	3.4	703	29	CG253039	CG253039	614	17	3.4	794	13	BU940170	BU940170	EINCS23TR
C 542	17	3.4	704	14	CB502332	CB502332	615	17	3.4	797	28	CC167022	CC167022	ii57g04.g
C 543	17	3.4	704	28	AZ876328	AZ876328	616	17	3.4	799	28	BZ608254	BZ608254	WHACS82TF
C 544	17	3.4	704	29	CC959506	CC959506	617	17	3.4	801	29	CG944105	CG944105	MBEAD20TR
C 545	17	3.4	706	12	BM577343	BM577343	618	17	3.4	802	10	BF786964	BF786964	602112159
C 546	17	3.4	708	13	BZ228539	BZ228539	619	17	3.4	807	13	BU120813	BU120813	603146753
C 547	17	3.4	709	28	BZ775841	ih96c11.g	620	17	3.4	815	28	BZ622692	BZ622692	ig80a12.b
C 548	17	3.4	710	13	BU208805	603103929	621	17	3.4	816	28	BZ398150	BZ398150	EINBQ14TR
C 549	17	3.4	710	13	BU399755	BU399755	622	17	3.4	822	29	CG951510	CG951510	MBEAD20TR
C 550	17	3.4	711	28	CC058353	CC058353	623	17	3.4	823	13	BU121914	BU121914	603146886
C 551	17	3.4	713	28	CG166803	CG166803	624	17	3.4	823	13	BU375433	BU375433	603598377
C 552	17	3.4	715	28	A0750578	HS_5573.B	625	17	3.4	825	13	BQ429536	BQ429536	AGENCOURT
C 553	17	3.4	720	13	BU121213	BU121213	626	17	3.4	826	10	BF238929	BF238929	601904567
C 554	17	3.4	720	29	EX174925	EX174925	627	17	3.4	828	29	CG675533	CG675533	OGNAGA1TH
C 555	17	3.4	721	12	BG856150	1024044G0	628	17	3.4	832	13	BU316638	BU316638	603486889
C 556	17	3.4	722	28	AZ913584	RPCT-24-1	629	17	3.4	832	13	CG952330	CG952330	MBENAL2TR
C 557	17	3.4	724	28	CG169171	ii91c01.g	630	17	3.4	836	29	CG970391	CG970391	ZUACF36TV
C 558	17	3.4	726	13	BU450823	BU450823	631	17	3.4	837	13	BU123728	BU123728	603148689
C 559	17	3.4	727	29	CC569220	CC569220	632	17	3.4	838	28	BH714331	BH714331	BOMCA20TR
C 560	17	3.4	731	13	BU253426	603414416	633	17	3.4	838	29	CG967781	CG967781	MBEDM57TF
C 561	17	3.4	731	13	BU291499	BU291499	634	17	3.4	842	28	CC415986	CC415986	PUHNM81TD
C 562	17	3.4	731	28	CC159501	CC159501	635	17	3.4	845	13	BU121156	BU121156	603145103
C 563	17	3.4	732	28	BZ618773	BZ618773	636	17	3.4	851	14	CB623797	CB623797	OS1fEa11M
C 564	17	3.4	734	9	AL701062	DKPZp6861	637	17	3.4	851	14	CK240334	CK240334	AGENCOURT
C 565	17	3.4	735	13	BU392015	BU392015	638	17	3.4	851	14	BU329317	BU329317	603493978
C 566	17	3.4	735	29	CB149937	CB149937	639	17	3.4	856	29	CG998742	CG998742	ZUABL25TH
C 567	17	3.4	736	13	BU290602	BU290602	640	17	3.4	857	10	BF382446	BF382446	601815423
C 568	17	3.4	737	13	BU291829	BU291829	641	17	3.4	862	29	CG938662	CG938662	MBELC89TR
C 569	17	3.4	738	28	AZ752985	RPCT-24-1	642	17	3.4	864	13	BU135318	BU135318	603488235
C 570	17	3.4	739	28	A0747827	HS_5537.A	643	17	3.4	867	13	BU265989	BU265989	603506544
C 571	17	3.4	741	13	BU122230	BU122230	644	17	3.4	871	29	CC478485	CC478485	CH240_305
C 572	17	3.4	741	13	BU741903	UI-E-B01	645	17	3.4	872	14	CA767499	CA767499	AF53-Rof
C 573	17	3.4	741	28	BZ325677	BZ325677	646	17	3.4	872	14	CF637738	CF637738	zmzww00_0
C 574	17	3.4	742	28	BZ041122	BZ041122	647	17	3.4	876	13	BZ093419	BZ093419	CH230-221
C 575	17	3.4	743	14	CD826681	BN25_064K	648	17	3.4	880	10	BF382575	BF382575	601815049
C 576	17	3.4	744	12	BG8339172	BG8339172	649	17	3.4	883	13	BU521307	BU521307	AGENCOURT
C 577	17	3.4	744	29	CG911778	CG911778	650	17	3.4	885	28	CC387720	CC387720	PUHF777TB
C 578	17	3.4	745	28	BZ130367	BZ130367	651	17	3.4	885	29	CC644421	CC644421	OGNAL02TV
C 579	17	3.4	746	13	BU122183	BU122183	652	17	3.4	887	13	BU292629	BU292629	603607977
C 580	17	3.4	746	14	CF251254	esa022.g0	653	17	3.4	891	28	BH696190	BH696190	BOMJ765TR
C 581	17	3.4	747	29	CG937373	CG937373	654	17	3.4	892	12	BG388328	BG388328	602413336
C 582	17	3.4	748	29	CG694179	CG694179	655	17	3.4	892	14	CA470555	CA470555	AGENCOURT
C 583	17	3.4	749	28	BH527904	BH527904	656	17	3.4	893	10	BE256713	BE256713	601115524
C 584	17	3.4	750	14	CB655364	CB655364	657	17	3.4	896	28	CC369248	CC369248	PUHFM58TB
C 585	17	3.4	751	9	AJ4444733	AJ4444733	658	17	3.4	901	28	BZ388271	BZ388271	EINCT95TR
C 586	17	3.4	753	11	CNS09K9K	BM062340	659	17	3.4	902	28	BH137615	BH137615	ENTNM60TR
C 587	17	3.4	757	28	BH497779	BOGN45TR	660	17	3.4	903	28	BH137615	BH137615	ENTNM60TR
C 588	17	3.4	759	28	BZ389059	EINBC33TR	661	17	3.4	910	29	CG768987	CG768987	TCB50_4.B

662 17 CG257223 CGWANO4TV 735 16 3.2 97 9 AV847224
663 17 CG169172 i191c01.g 736 16 3.2 112 9 AV844954
664 17 AZ544572 ENTGS50TR 737 16 3.2 113 14 CF008086
665 17 CD387633 AGENCOURT 738 16 3.2 117 29 CG628723
666 17 BQ939200 AGENCOURT 739 16 3.2 119 29 CG119563
667 17 BU238656 603321612 740 16 3.2 123 14 H75155
668 17 BU386900 603583073 741 16 3.2 126 28 BZ097052
669 17 CK022899 AGENCOURT 742 16 3.2 127 14 T81173
670 17 BF159387 601770366 743 16 3.2 130 9 AV841415
671 17 CC169251 PUHEW58TD 744 16 3.2 136 9 AV853453
672 17 CC173240 ZMMBSC029 745 16 3.2 141 12 BI435783
673 17 BZ989874 PUGK629TD 746 16 3.2 146 28 AF087214
674 17 BQ961489 AGENCOURT 747 16 3.2 149 29 BX533493
675 17 BU155487 AGENCOURT 748 16 3.2 147 9 AV906325
676 17 CG854814 ZMMBSC022 749 16 3.2 147 28 AZ658007
677 17 BE779404 601464122 750 16 3.2 155 14 CF004412
678 17 BH139313 ENTN883TR 751 16 3.2 157 29 AV245174
679 17 BH150344 ENTQ03TR 752 16 3.2 162 14 AA011781
680 17 CG921118 MBELB02TR 753 16 3.2 167 14 D3569421
681 17 BQ679951 AGENCOURT 754 16 3.2 167 14 D35116
682 17 CF581561 AGENCOURT 755 16 3.2 170 13 BQ376545
683 17 CB587633 AGENCOURT 756 16 3.2 176 13 BW067379
684 17 CG257210 CGWANO4TH 757 16 3.2 177 13 BU802796
685 17 AQ573548 ndxb0082L 758 16 3.2 178 13 BU465547
686 17 BU772153 SUEEMH12 759 16 3.2 178 13 BW121856
687 17 CG771931 TCB48.1.A 760 16 3.2 178 13 BW121856
688 17 BX042931 Single Ie 761 16 3.2 180 13 BW110232
689 17 CG603528 OGULI47TV 762 16 3.2 182 9 AV986588
690 17 BX062341 Single re 763 16 3.2 182 10 BF758048
691 17 BU726460 AGENCOURT 764 16 3.2 183 10 BE432930
692 17 AL277353 Tetraodon 765 16 3.2 184 12 BP014336
693 17 CG854801 ZMMBSC022 766 16 3.2 185 9 AI481498
694 17 AV003929 AV003929 767 16 3.2 186 10 BE693913
695 17 CC419750 PUHQL88TD 768 16 3.2 186 14 CD856278
696 17 BE891673 601484576 769 16 3.2 189 10 CD856278
697 17 BF242265 601879412 770 16 3.2 189 29 CE648647
698 17 BU908899 AGENCOURT 771 16 3.2 199 9 AU493823
699 17 CG675541 CGNAG41TV 772 16 3.2 199 9 AV893469
700 17 AV078077 AV078077 773 16 3.2 200 9 AA031030
701 17 BX042930 Single re 774 16 3.2 200 14 H54900
702 17 BU468665 603212004 775 16 3.2 200 29 CG918828
703 17 BZ394988 EINCX59TR 776 16 3.2 202 10 BB184914
704 17 AL301045 Tetraodon 777 16 3.2 202 9 AI340753
705 17 BG392743 602410111 778 16 3.2 203 29 CG815804
706 17 CG271552 CH261-90K 779 16 3.2 204 9 AV164036
707 17 AL178692 Tetraodon 780 16 3.2 204 10 BB133448
708 17 BU121598 603145372 781 16 3.2 205 14 D42715
709 17 AL431501 T3 end of 782 16 3.2 205 14 AW428727
710 17 CC259349 CH261-164 783 16 3.2 206 10 AA390329
711 17 AL071318 Drosophil 784 16 3.2 207 9 BA29632
712 17 AL431296 T3 end of 785 16 3.2 207 13 C24166
713 17 BE543554 601070527 786 16 3.2 210 9 AI5782176
714 17 CG388249 ZMMBSC056 787 16 3.2 211 9 BB237383
715 17 CK206027 FGAS02114 788 16 3.2 211 10 BB237383
716 17 CK206027 FGAS01760 789 16 3.2 213 9 AV855362
717 17 CC263856 CH261-49L 790 16 3.2 213 13 BQ376546
718 17 CC203665 CH261-34L 791 16 3.2 214 14 CF474295
719 17 CC274272 CH261-510 792 16 3.2 215 9 AV862839
720 17 CC207844 CH261-700 793 16 3.2 216 9 AV839325
721 17 CC184077 CH261-140 794 16 3.2 216 9 AA472125
722 17 BF134511 601784917 795 16 3.2 217 10 CF330248
723 17 CB941941 AGENCOURT 796 16 3.2 217 10 AW273976
724 17 CC309666 TAM32-23G 797 16 3.2 218 9 AV867567
725 17 BQ721007 AGENCOURT 798 16 3.2 218 9 AV867567
726 17 CC305301 CH261-2N2 799 16 3.2 218 9 AV867567
727 17 CG754285 F049-3-F1 800 16 3.2 218 9 AV867567
728 17 BM926222 AGENCOURT 801 16 3.2 218 9 AV867567
729 17 AK035539 Mus muscu 802 16 3.2 218 9 AV867567
730 17 AK088565 Mus muscu 803 16 3.2 218 9 AV867567
731 17 AK075594 Mus muscu 804 16 3.2 218 9 AV867567
732 17 AK030815 Mus muscu 805 16 3.2 218 9 AV867567
733 17 AV852625 AV852625 806 16 3.2 218 9 AV867567
734 17 AV852625 AV852625 807 16 3.2 218 9 AV867567


```

/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6517548"
/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/notes="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

```

ORIGIN

```

Query Match      4.2%; Score 21; DB 13; Length 973;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 55 GAGAGAGCCACCATTTGGC 75
    |||||
Db 833 GAGAGAGCCACCATTTGGC 853

```

RESULT 3

```

CE545692
LOCUS      213 bp DNA linear GSS 28-SEP-2003
DEFINITION tigr-gss-dog-17000366132442 Dog Library Canis familiaris genomic,
genomic survey sequence.

```

```

ACCESSION CE545692
VERSION   1
KEYWORDS  GSS
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris

```

REFERENCE

```

AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
            1 (bases 1 to 213)
            Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
            Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
            Venter, J.C.

```

```

TITLE      The dog genome: survey sequencing and comparative analysis

```

```

JOURNAL    Science 301 (5641), 1898-1903 (2003)
MEDLINE    22875432
PUBMED     14512627

```

COMMENT

```

Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

```

FEATURES

```

source
1..213
    Location/Qualifiers
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from
        peripheral blood"

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 29; Length 213;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 269 CCATATTGATCATCTTGGC 288
    |||||
Db 190 CCATATTGATCATCTTGGC 209

```

RESULT 4

```

AQ959051/c
LOCUS      346 bp DNA linear GSS 28-JAN-2000
DEFINITION LEREG96TR LERE Arabidopsis thaliana genomic clone LEREG96, genomic

```

```

survey sequence.
ACCESSION AQ959051
VERSION   AQ959051.1
KEYWORDS  GI:6786752
SOURCE    GSS.
ORGANISM  Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsi.
          1 (bases 1 to 346)
          Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,
          Feldhym, T., Liang, F., Creasy, T. and Fraser, C.M.
          Genomic survey sequencing of Landsberg erecta ecotype of
          Arabidopsis thaliana and identification of sequence-based
          polymorphisms
          Unpublished (2000)
          Contact: Xiaoying Lin
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 0200
          Fax: 301 838 0208
          Email: at@tigr.org
          For additional information, see http://www.tigr.org/cdb/at/at.html
          Seq primer: TR
          Class: shotgun.

```

FEATURES

```

source
1..346
    Location/Qualifiers
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /strain="LANDSBERG ERECTA"
        /db_xref="taxon:3702"
        /clone="LEREG96"
        /clone_lib="LERE"
        /note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was
        sheared to 0.6-0.8 Kbp before ligation."

```

ORIGIN

```

Query Match      4.0%; Score 20; DB 28; Length 346;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 345 TTTTCAACAAAAATAACAC 364
    |||||
Db 99 TTTTCAACAAAAATAACAC 80

```

RESULT 5

```

CA912211/c
LOCUS      360 bp mRNA linear EST 27-DEC-2002
DEFINITION PCS02658 Scarlet Runner Bean Suspensor Region TriplEx2 Phaseolus
coccineus cDNA 5' similar to Putative protein (NM_118618), mRNA
sequence.

```

```

ACCESSION CA912211
VERSION   CA912211.1
KEYWORDS  GI:27399203
SOURCE    EST.
ORGANISM  Phaseolus coccineus
          Phaseolus coccineus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Phaseolus.

```

REFERENCE

```

AUTHORS    1 (bases 1 to 360)
            Bui, A.Q., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S.,
            McElroy, K.E., Choi, P.S., Harada, J.J., Fischer, R.L. and
            Goldberg, R.B.

```

TITLE

```

Gene Activity in Different Regions of a Post-Fertilization Plant
Embryo by EST Analysis

```

JOURNAL

```

COMMENT    Unpublished (2002)
            Contact: Goldberg, R.B.
            Department of Molecular, Cell, & Developmental Biology
            University of California, Los Angeles
            621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
            Tel: 310 825 3270

```

Fax: 310 825 8201
Email: bobg@cla.edu
Seq primer: 5' Triplex
POLYA-No.

FEATURES

source Location/Qualifiers

1. .360
/organism="Phaseolus coccineus"
/mol_type="mRNA"
/cultivar="Hammond's Dwarf Scarlet"
/db_xref="taxon:3886"
/dev_stage="6-days post-pollination"
/clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
/note="Organ: Suspensor Region of Globular-Stage Embryos;
Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Suspensor
regions were micro-dissected from globular-stage embryos
six days after pollination from greenhouse-grown plants
[Weterings et al., Plant Cell 13, 2409-2425 (2001)].
Double-stranded cDNA was synthesized from suspensor mRNA
using the SMART cDNA Library Construction Kit according to
the manufacturer (Clontech). The suspensor cDNA fragments
were directionally ligated into the SfiI restriction site
of the lambda Triplex2 vector (Clontech), and the
recombinant cDNAs were transformed into E. coli XL1-Blue
cells (Clontech). Suspensor cDNA plasmids used for
directional sequencing were obtained by in vivo excision
from the lambda Triplex2 recombinants in E. coli BM25.8
cells (Clontech)."

ORIGIN

Query Match 4.0%; Score 20; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCACAAAAATAACACTTGG 368
|||||
Db 300 TCACAAAAATAACACTTGG 281

RESULT 6

BM892066/c
LOCUS 333 bp mRNA linear EST 11-MAR-2002
DEFINITION sam47h05.y1 Gm-cl069 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl069-2673 5' similar to TR:081286 O81286 T14P8.7 PROTEIN. ;,
mRNA sequence.

ACCESSION BM892066
VERSION BM892066.1 GI:19347186
KEYWORDS Glycine max (soybean)
SOURCE Glycine max

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 393)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)

TITLE Contact: Shoemaker R/Public Soybean EST Project
JOURNAL Public Soybean EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Putative full length read
vector to vector length is 394
Seq primer: -40RP from Gibco.

FEATURES

source Location/Qualifiers

1. .393
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl069-2673"
/tissue_type="Degenerating cotyledons, 9-10 day old
etiolated seedling"
/lab_host="DH10B"
/clone_lib="Gm-cl069"
/note="Vector: pluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

ORIGIN

Query Match 4.0%; Score 20; DB 12; Length 393;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCACAAAAATAACACTTGG 368
|||||
Db 174 TCACAAAAATAACACTTGG 155

RESULT 7

AU203244 490 bp mRNA linear EST 17-JUL-2001
LOCUS AU203244 unpublished oligo-capped cDNA library, stage L2
DEFINITION Caenorhabditis elegans cDNA clone yk818c06 5', mRNA sequence.

ACCESSION AU203244
VERSION AU203244.1 GI:14833741
KEYWORDS EST.
SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 490)
Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
A complementary view of the C.elegans genome
Unpublished (2001)

TITLE Contact: Yuji Kohara
JOURNAL Genome Biology Lab.
COMMENT National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers

FEATURES

source
1. .490
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk818c06"
/sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L2"
/clone_lib="unpublished oligo-capped cDNA library, stage
L2"

ORIGIN

Query Match 4.0%; Score 20; DB 9; Length 490;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 TTTCAACAAAAATAACACTT 366
 |||||
 Db 443 TTTCAACAAAAATAACACTT 462

RESULT 8
 AV960301
 LOCUS
 DEFINITION AV960301 Nori Satoh unpublished cDNA library, cleavage stage embryo
 Ciona intestinalis cDNA clone c1c12a15 5', mRNA sequence.
 ACCESSION AV960301.1 GI:19448600
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Ciona intestinalis
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Clonidae; Ciona.
 1 (bases 1 to 539)
 Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
 Expressed genes in Ciona intestinalis
 Unpublished (2000)
 JOURNAL
 COMMENT
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source
 1..539
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="c1c12a15"
 /tissue_type="whole animal"
 /dev_stage="cleavage stage embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, cleavage stage embryo"

ORIGIN

Query Match 4.0%; Score 20; DB 9; Length 539;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AAGCTCTTGCTGATTTCTG 450
 |||||
 Db 211 AAGCTCTTGCTGATTTCTG 230

RESULT 9
 BW204471
 LOCUS
 DEFINITION BW204471 Nori Satoh unpublished cDNA library, cleavage stage embryo Ciona
 intestinalis cDNA clone c1c1087m01 5', mRNA sequence.
 ACCESSION BW204471
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Ciona intestinalis
 Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Clonidae; Ciona.
 1 (bases 1 to 541)
 Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
 Expressed genes in Ciona intestinalis (2002c)
 Unpublished (2002)
 JOURNAL
 COMMENT
 Department of Zoology

Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: sato@ascidian.zool.kyoto-u.ac.jp.

FEATURES

source
 1..541
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="c1c1087m01"
 /tissue_type="whole body"
 /dev_stage="cleaving embryo"
 /clone_lib="Nori Satoh unpublished cDNA library, cleaving embryo"

ORIGIN

Query Match 4.0%; Score 20; DB 13; Length 541;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 AAGCTCTTGCTGATTTCTG 450
 |||||
 Db 221 AAGCTCTTGCTGATTTCTG 240

RESULT 10

BMS21341/c
 LOCUS
 DEFINITION BMS21341 Y1 Gm-c1057 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-c1057-5254 5', similar to TR:O81286 O81286 T14P8.7 PROTEIN. ;
 mRNA sequence.

ACCESSION BMS21341
 VERSION BMS21341.1 GI:18692493
 KEYWORDS
 SOURCE
 ORGANISM

Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 551)
 AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
 Beck, C., Wylie, I., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
 Bowers, J., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT

Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact: ccu@resgen.com web site:
 www.resgen.com

Seq primer: -40RP from Gibco
 High quality sequence stop: 421.

FEATURES

source
 1..551
 /organism="Glycine max"
 /mol_type="mRNA"
 /db_xref="taxon:3847"
 /clone="SOYBEAN CLONE ID: Gm-c1057-5254"
 /tissue_type="Degenerating cotyledons, 2 week old seedling"
 /lab_host="DH10B"
 /clone_lib="Gm-c1057"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 2 week old seedlings from P1468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

ORIGIN

Query Match 4.0%; Score 20; DB 12; Length 551;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 349 TCAACAAAATAACACTTGG 368
Db 367 TCAACAAAATAACACTTGG 348

RESULT 11

BI944599/c

LOCUS

DEFINITION

ID: Gm-cl062-2952 5' similar to TR:081286 O81286 T14P8.7 PROTEIN.

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Comment

Features

Source

Source

Source

Source

Source

Source

Source

Source

Source

Source

Source

Source

Source

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```

ORGANISM      Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 574)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
1. 574
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-cl052-7225"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
/clone_lib="Gm-cl052"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 1
week old greenhouse grown plants. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site and a 3'
anchor. EcoRI adapters were ligated to the blunt-ended
cDNA fragments followed by XhoI digestion. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(GibcoBRL). The library was constructed in cooperation
with Dr. Paul Keim's laboratory at Northern Arizona
University."

ORIGIN
Query Match      4.0%; Score 20; DB 13; Length 574;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 TCACAAAAATAACACTTGG 368
|||||
Db 164 TCACAAAAATAACACTTGG 145

RESULT 14
BI943495/c
LOCUS
DEFINITION
sp95c04.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl045-1375 5' similar to TR:081286 081286 T14P8.7 PROTEIN. ;
mRNA sequence.
ACCESSION
BI943495
VERSION
BI943495.1 GI:16279552
KEYWORDS
EST.

ORGANISM      Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 577)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 425.
Location/Qualifiers
1. 577
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl045-1375"
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/clone_lib="Gm-cl045"
/notes="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:
XhoI; This cDNA library was constructed from mRNA isolated
from etiolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) primer with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by digestion with EcoRI and XhoI. The cDNA
fragments were directionally cloned into the EcoRI-XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(Gibco BRL). This library was constructed by Dr. Randy
Shoemaker."

ORIGIN
Query Match      4.0%; Score 20; DB 12; Length 577;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 TCACAAAAATAACACTTGG 368
|||||
Db 333 TCACAAAAATAACACTTGG 314

RESULT 15
AZ493804
LOCUS
DEFINITION
1M0328K07R Mouse 10kb plasmid UGCGM library Mus musculus genomic
clone UGCG1M0328K07 R, genomic survey sequence.
ACCESSION
AZ493804
VERSION
AZ493804.1 GI:10667826
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)

```

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0328 row: K column: 07
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.

FEATURES
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1..581
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/sex="Male"
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/clone_lib="Mouse 10Kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWP42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 4.0%; Score 20; DB 28; Length 581;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 434 CTCTTGCTGATTTCTGAGC 453
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Job time : 2464 secs